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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
Art Unit: _____ Phone Number 30 _____ Serial Number: _____
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
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jan.delaval@uspto.gov

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Searcher Phone #: 4498
Searcher Location: _____
Date Searcher Picked Up: 2/8/03
Date Completed: 2/8/03
Searcher Prep & Review Time: _____
Clerical Prep Time: 15
Online Time: 10

Type of Search

NA Sequence (#) _____
AA Sequence (#) ☒ _____
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

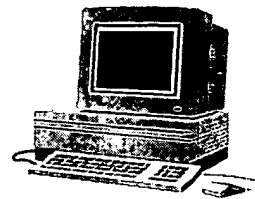
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BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information Center

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-Chem searcher* who conducted the search *or contact*:

Mary Hale, Supervisor, 308-4258
CM-1 Room 1E01

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the **Circulation Desk CM-1**, or send to Mary Hale, **CM1-1E01** or e-mail **mary.hale@uspto.gov**.

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:28:18 ; Search time 14 Seconds
(without alignments)
34.334 Million cell updates/sec

Title: US-09-251-073A-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 73.*
1: piri.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
---------------	-------	----------------	--------	-------	-------------

No matches found

Search completed: February 8, 2003, 10:30:21
Job time : 14 secs

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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:25:23 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-251-073A-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
---------------	-------	----------------	--------	-------	-------------

No matches found

Search completed: February 8, 2003, 10:29:25
Job time : 11 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:27:53 ; Search time 28 Seconds
(without alignments)
36.794 Million cell updates/sec

Title: US-09-251-073A-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : SPTREMBL 21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
---------------	----------------	--------------	----	-------------

No matches found

Search completed: February 8, 2003, 10:30:00
Job time : 28 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2003, 10:25:08 ; Search time 33. Seconds
(without alignments)
20.189 Million cell updates/sec

Title: US-09-251-073a-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 11

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database :			
A_Geneseq_101002.*			
1:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*		
2:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*		
3:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*		
4:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*		
5:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*		
6:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*		
7:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*		
8:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*		
9:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*		
10:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*		
11:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*		
12:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*		
13:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*		
14:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*		
15:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*		
16:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*		
17:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*		
18:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*		
19:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*		
20:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*		
21:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*		
22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*		
23:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	5	17	Alpha-4Beta-1 inte
2	23	100.0	5	18	LDV-peptide capabl
3	23	100.0	5	19	Peptide recognised
4	23	100.0	5	20	Integrin ligand di
5	23	100.0	5	21	Cell adhesion pept
6	23	100.0	5	21	Fibronectin CSI-de
7	23	100.0	5	21	VLA-4 inhibitor pe
8	23	100.0	5	22	Fibronectin VLA-4
9	23	100.0	5	22	Fibronectin fragme
10	23	100.0	5	22	Integrin recogniti

11 23 100.0 5 22 AAB59135 Peptide #3 recogni

ALIGNMENTS

RESULT 1
AAR95719
ID AAR95719 standard; peptide; 5 AA.
XX
XX AAR95719;
XX
XX 04-DEC-1996 (first entry)
XX
XX Alpha-4Beta-1 integrin binding inhibitory peptide 16.
XX
XX VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
XX inhibitor; binding; white blood cell; migration; capillary wall;
XX tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
XX CSI; CS5; HI; LDV; active site.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 5 /note= "Val-NH2"
XX
XX US5510332-A.
XX
XX 23-APR-1996.
XX
XX 07-JUL-1994; 94US-0271830.
XX
XX 07-JUL-1994; 94US-0271830.
XX
XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
XX
XX Beck PJ, Kogan TP, Ren K, Vanderslice P;
XX WPI; 1996-221274/22.
XX
XX New peptide(s) based on the LDV domain of fibronectin - used for
XX inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
XX fibronectin or invasin
XX
XX Disclosure; Column 21-22; 35pp; English.
XX
XX Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
XX surface of endothelial cells that line the interior wall of capillaries.
XX VCAM-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
XX VLA-4 for very late antigen-4), a heterodimeric protein present on the
XX surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
XX white blood cells to adhere to the capillary wall in areas where the
XX tissue surrounding the capillary has been infected or damaged. Sometimes
XX this white blood cell migration can become uncontrolled, with white
XX blood cells flooding to the scene, causing widespread tissue damage.
XX Cgds. capable of blocking this process may be beneficial as therapeutic
XX agents. IA4B1 also recognises the extracellular matrix glycoprotein
XX fibronectin. Three distinct IA4B1-binding sites have been identified
XX within fibronectin. One site is found in the HeplI region and is
XX expressed in all isoforms; two others (CSI and CS5) are present in the
XX alternatively spliced type III connecting segments. CSI has the higher
XX affinity for IA4B1 and contains the tripeptide LDV as its minimal active
XX site. Peptides AAR95704-805 are modeled after a portion of the CSI
XX peptide that include the LDV domain presented in such a way by its novel
XX flanking sequence to produce a potent inhibitor of IA4B1 binding.
XX
XX Sequence 5 AA;
XX
XX Query Match 100.0%; Score 23; DB 17; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
XX Matches 5; Conservative 0; Mismatches 0;

```

Qy 1 EILDV 5
    |||||
Db 1 EILDV 5

RESULT 2
AAW25192
ID AAW25192 standard; peptide; 5 AA.
XX
AC AAW25192;
XX
DT 05-JAN-1998 (first entry)
XX
DE LDV-peptide capable of binding cell adhesion molecules.
XX
KW LDV; leucine; aspartic acid; valine; cell adhesion molecule;
KW binding; bladder irrigation; tumour removal; endoscopic operation;
KW transurethral resection; cancer; neoplasia.
XX
OS Synthetic.
XX
PN DEL9529909-AL.
XX
PD 20-FEB-1997.
XX
PF 15-AUG-1995; 95DE-1029909.
XX
PR 15-AUG-1995; 95DE-1029909.
XX
PA (PREP ) FRESSENIUS AG.
XX
PI Boehle A;
XX
DR WPI; 1997-133793/13.
XX
PT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
PT adhesion molecules
XX
PS Claim 6; Page 8; 8pp; German.
XX
AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
CC The peptides are capable of binding to cell adhesion molecules and
CC are used in aqueous irrigation solutions for use during and after
CC endoscopic operations. Preferred irrigation solutions are
CC electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
CC oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
CC GRPP, VTL, YIGSR, KOAGDV and/or REDV (given in one letter amino acid
CC code). The solutions are especially used for irrigating the bladder
CC during and after tumour removal by transurethral resection. The
CC peptides protect against recurrence of tumours.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
    |||||
Db 1 EILDV 5

RESULT 3
AAW46318
ID AAW46318 standard; Protein; 5 AA.
XX
AC AAW46318;
XX
DT 08-MAY-1998 (first entry)
XX
DE Peptide recognised by integrin alpha4etal.
XX
KW Fibrinogen; integrin; alpha-IIB-beta3; cell surface receptor;

Qy 1 EILDV 5
    |||||
Db 1 EILDV 5

RESULT 4
AAV03855
ID AAV03855 standard; peptide; 5 AA.
XX
AC AAV03855;
XX
DT 16-JUN-1999 (first entry)
XX
DE Integrin ligand dissociator (ILD) peptide.
XX
KW Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke;
KW fibrinogen; glycoprotein IIB-IIIa; angina; myocardial infarction; bone;
KW osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
KW psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
KW organ transplant rejection; arthritis; ILD.
XX
OS Synthetic.
XX
PN WO9911280-A1.

```

penton base protein; coat proteins; adenovirus; binding site;
 cellular adhesion; extracellular matrix molecule; binding domain;
 cell surface binding site; bispecific molecule; gene therapy.

Unidentified.
 US5712136-A.
 27-JAN-1998.
 17-APR-1996; 96US-0634060.
 08-SEP-1994; 94US-0303162.
 (GENV-) GENVEC INC.
 Brough DE, Bruder JT, Kovsesi I, McVey DL, Roelvink PW;
 Wickham TJ;
 WPI; 1998-119984/11.
 Methods for introducing adenovirus into cells - used for genetic
 engineering and gene therapy
 Claim 27; Column 2; 56pp; English.
 The present sequence is a linear stretch of amino acids (present in
 fibronectin) recognised by the integrin alpha4beta1. Integrins are
 cell surface receptors. The penton base protein (one of the coat
 proteins) of adenoviruses binds to integrins. The integrins not only
 provide a binding site for the adenoviral penton base protein, but also
 mediate cellular adhesion to the extracellular matrix molecules. The
 specification describes a method of introducing an adenovirus into
 a cell in vitro having a particular cell surface binding site. The
 adenovirus is contacted with a bispecific molecule comprising a component
 that selectively binds a binding domain of the penton base protein of the
 adenovirus and a second component that selectively binds the cell surface
 binding site. A complex of the adenovirus and the bispecific molecule is
 formed, and the cell is contacted with it to allow entry of the
 adenovirus into the cell. The methods can be used for research and the
 vectors can be used for gene therapy.

Query Match 100.0%; Score 23; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 |||||
 Db 1 EILDV 5

PD 11-MAR-1999.
XX
PF 03-SEP-1998; 98WO-US18305.
XX
PR 03-SEP-1997; 97US-0057463.
XX
PA (BURN-) BURNHAM INST.
XX
PI Hu DD, Smith JW;
XX
XX WPI; 1999-243586/20.
XX
XX Disaggregating a ligand: integrin receptor complex
XX
XX Disclosure; Page 10; 39pp; English.
XX
XX The invention relates to integrin ligand dissociators. Disaggregation of
CC an existing platelet thrombus in a blood vessel is due to dissociation of
CC fibrinogen from glycoprotein IIb-IIIa. This dissociation is caused by the
CC binding of an integrin-ligand dissociator at ligand binding site I of
CC glycoprotein IIb-IIIa. The invention provides a method of disaggregating
CC an existing platelet thrombus in a blood vessel, where the platelet
CC thrombus may form an occlusion of a blood vessel, in a subject comprises
CC administering a compound which dissociates fibrinogen bound to a first
CC site on platelet glycoprotein IIb-IIIa, by binding to a second
CC interacting site on platelet glycoprotein IIb-IIIa, disaggregating the
CC platelet thrombus. The method is used to treat humans with unstable
CC angina, stroke and/or acute myocardial infarction. The methods can be
CC used to enact de-adhesion of osteoclasts from the bone surface to halt
CC bone loss in a patient with osteoporosis. The methods can also be used
CC for the de-adhesion of angiogenic endothelial cells in a patient with a
CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
CC retinopathy, psoriasis. The methods can also be used to treat tumours,
CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
CC bowel disease, or organ transplant rejection, and asthma. The methods can
CC be used for the dissolution of pre-formed platelet aggregates, which is a
CC departure from the current strategy of treatment prior to formation of
CC vascular occlusions. The present sequence represents an integrin ligand
CC dissociator (ILD) that can be used in the method of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
| | | | |
DB 1 EILDV 5

RESULT 5
AAY80488
ID AAY80488 standard; peptide; 5 AA.
XX
AC AAY80488;
XX
DT 06-JUN-2000 (first entry)
XX
DE Cell adhesion peptide #23.
XX
KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
XX
OS Synthetic.
XX
XX WO200004941-A1.
XX
XX 03-FEB-2000.
XX
XX 22-JUL-1999; 99WO-US16800.
XX

PR 24-JUL-1998; 98US-0122348.
XX
PA (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
XX
PI Budny JA;
XX
XX WPI; 2000-195084/17.
XX
XX System for reconstructing osseous tissue, useful e.g. for treating
PT fractures, comprises scaffold containing promoter of bone formation and
PT inhibitor of bone resorption -
XX
XX Claim 14; Page 32; 44pp; English.
XX
XX The invention relates to a novel system for reconstitution of osseous
CC tissue comprising a scaffold carrying a compound (I) that promotes
CC bone formation and a component that decreases bone resorption (II).
CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
CC matrix. (I) is preferably selected from: selectin or selectin binding
CC fragments, proteins and peptides that facilitate cell adhesion,
CC plasminogen activator inhibitors, protease inhibitors and
CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed
CC examples of cell adhesion peptides used in the system of the invention.
CC The system is used to replace, remodel or correct bone defects, e.g.
CC fractures, fissures or bone mass loss. Incorporation of (I) into the
CC scaffold results in rapid seeding by osteoblasts and the development of
CC an organic matrix, i.e. the preformed scaffold replaces the
CC rate-determining step of extracellular matrix formation. The scaffold can
CC be designed to have a predetermined resorption/degradation rate, and may
CC include regulatory compounds for specific cell types.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 21; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
| | | | |
DB 1 EILDV 5

RESULT 6
AAY77442
ID AAY77442 standard; peptide; 5 AA.
XX
AC AAY77442;
XX
DT 22-MAY-2000 (first entry)
XX
DE Fibronectin CSI-derived peptide #33.
XX
KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
KW CD49G/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
XX
OS Mammalia.
XX
XX WO200002903-A1.
XX
XX 20-JAN-2000.
XX
XX 15-DEC-1998; 98WO-US26605.
XX
XX 10-JUL-1998; 98US-0113689.
XX
XX (CYTE-) CYTEL CORP.
XX
XX Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
XX WPI; 2000-182213/16.
XX

PT New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders -
 XX
 XX Disclosure; Fig 2; 243pp; English.

XX The invention relates to peptidomimetic compounds (AAV77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAV77411-Y77414
 CC and AAV77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAV77410).

XX
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 23; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 7
 AAY69619
 ID AAY69619 standard; peptide; 5 AA.
 AC AAY69619;
 XX
 XX 19-APR-2000 (first entry)
 DT
 DE VLA-4 inhibitor peptide #2.
 XX
 XX LDV peptide; VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
 KW CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative;
 KW arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder;
 KW autoimmune disorder; respiratory disorder; LDV motif.
 XX
 OS Synthetic.
 XX
 XX WO200000477-A1.
 XX
 XX 06-JAN-2000.
 XX
 XX 31-MAY-1999; 99WO-IB00973.
 PF
 XX 30-JUN-1998; 98US-0091180.
 XX
 XX (PFIZ) PFIZER PROD INC.
 PA
 XX Duplantier AJ, Milici AJ, Chupak LS;
 XX WPI; 2000-126762/11.
 XX

PT Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives -
 XX
 XX Disclosure; Page 2; 120pp; English.

XX The invention relates to novel arylalkyl and arylureidoalkyl
 CC azolylalkanoic acid derivatives and related compounds (I), and their
 CC salts and prodrugs. These are are integrin inhibitors, specifically of
 CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
 CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
 CC inducible cell surface protein VCAM-1 (vascular cell adhesion
 CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
 CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
 CC and consequent or associated pathogenic processes mediated by VLA-4, and
 CC may therefore be useful in the treatment and prevention of inflammatory,
 CC autoimmune, or respiratory disorders. These include asthma, arthritis,
 CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
 CC inflammatory bowel disease. Sequences AAY69618-Y69620 represent peptides
 CC derived from the VLA-4-binding domain of the FN CS-1 region which
 CC contain the LDV motif and are known to inhibit fibronectin-dependent
 CC cell adhesion.

XX
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 23; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 8
 AAB73465
 ID AAB73465 standard; peptide; 5 AA.
 XX
 XX AAB73465;
 AC
 XX 02-JUL-2001 (first entry)
 DT
 DE Fibronectin VLA-4 binding domain-derived pentapeptide #1.
 XX
 XX Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
 KW very late antigen; antibody; kidney disease; chronic renal failure;
 KW end-stage renal disease; chronic diabetic nephropathy;
 KW diabetic glomerulopathy; diabetic renal hypertrophy;
 KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
 KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
 KW nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
 XX
 OS Unidentified.
 XX
 XX WO200119396-A1.
 XX
 XX 22-MAR-2001.
 PD
 XX 14-SEP-2000; 2000WO-US25140.
 PF
 XX 14-SEP-1999; 99US-0153826.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
 PA
 XX Allen A, Pusey C, Lobb R;
 PI WPI; 2001-273408/28.
 XX
 XX Treating a mammal in, or at a risk of developing, chronic renal
 PT failure, involves administering at least one integrin antagonist to the
 PT mammal -
 XX
 XX Disclosure; Page 24; 62pp; English.
 PS
 XX

CC The invention relates to a method for treating a mammal with,
 CC or at risk of developing, chronic renal failure, involving the
 CC administration of at least one integrin antagonist. The integrin
 CC antagonists that may be used in the method include antagonists of
 CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
 CC containing integrins. In particular, the antagonists are antibodies
 CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
 CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
 CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
 CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
 CC The method of the invention may be used to treat chronic renal failure,
 CC end-stage renal disease, chronic diabetic nephropathy, diabetic
 CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
 CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
 CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
 CC peptides derived from the VLA-4 binding domain (CS-1 region) of
 CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
 CC therefore be used in the method of the invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 1 EILDV 5
 |||||

RESULT 9

AAB91966
 ID AAB91966 standard; Peptide; 5 AA.

XX
 AC AAB91966;

DT 22-JUN-2001 (first entry)

DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX WO200069900-A2.

PN 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

PF 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT

XX Disclosure; Page 569; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 1 EILDV 5
 |||||

RESULT 10

AAB50876

ID AAB50876 standard; peptide; 5 AA.

XX
 AC AAB50876;

DT 19-MAR-2001 (first entry)

DE Integrin recognition peptide sequence #3.

KW Integrin; transmembrane protein; alpha4 integrin inhibitor;
 KW paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
 KW multiple sclerosis; asthma; atherosclerosis; wound healing.

XX Unidentified.

PN WO200073342-A1.

PD 07-DEC-2000.

PF 01-JUN-2000; 2000WO-US15153.

PR 01-JUN-1999; 99US-0323447.

XX (SCRI) SCRIPPS RES INST.

XX Ginsberg MH, Pfaff M, Liu S;

XX WPI; 2001-070959/08.

PT Polypeptides useful in construction of structural models for
 PT identifying therapeutic compounds, comprises series of heptad repeats
 PT that mimic a transmembrane domain and cytoplasmic domain attached to
 PT heptad repeats

XX Disclosure; Page 2; 37pp; English.

XX The present sequence is given in a specification relating to a
 CC polypeptide comprising a series of heptad-repeats that mimic a
 CC transmembrane domain, and a selected cytoplasmic domain attached to the
 CC heptad repeats. At least a portion of the polypeptide is prepared
 CC recombinantly or at least 1 heptad repeat in the series has a different
 CC amino acid sequence to other heptad repeats in the series. The
 CC polypeptide is useful in the construction of structural models which are
 CC useful for evaluating structure and activity of a selected occupied and
 CC clustered transmembrane protein having the selected cytoplasmic domain
 CC and for identifying therapeutic compounds. It is also useful for
 CC identifying agents as inhibitors of alpha4 integrin biological

CC responses by contacting the structural model with paxillin or a
 CC paxillin related molecule in the presence and absence of a test agent
 CC and determining binding of paxillin or paxillin related molecule to the
 CC structural model. A decrease in binding in the presence of the test
 CC agent indicates that the test agent is an inhibitor of alpha4 integrin
 CC biological response. Inhibitors of the binding of paxillin to alpha4 are
 CC useful in blocking immune responses in conditions such as inflammatory
 CC bowel disease, arthritis, multiple sclerosis and asthma and in
 CC inhibiting atherosclerosis and scarring during wound healing.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 1 EILDV 5

RESULT 11

AAB59135
 ID AAB59135 standard; peptide; 5 AA.

XX AC AAB59135;

DT 21-MAR-2001 (first entry)

XX Peptide #3 recognised by integrin.

DE Heptad repeat; transmembrane domain; cytoplasmic; integrin;
 KW inflammation; thrombosis; malignancy.

XX Synthetic.

XX WO200073341-A1.

XX PD 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14656.

XX 27-MAY-1999; 99US-0320907.

XX (SCRI) SCRIPPS RES INST.

XX Ginsberg MH, Pfaff M;

XX WPI; 2001-041143/05.

XX Polypeptides useful in construction of structural models for
 PT identifying therapeutic compounds, comprises series of heptad repeats
 PT that mimic a transmembrane domain and cytoplasmic domain attached to
 PT the repeats -

XX Disclosure; Page 2; 36pp; English.

XX The present invention relates to a peptide with a series of
 CC heptad-repeats that mimic a transmembrane domain and a selected
 CC cytoplasmic domain attached to the heptad repeats. The invention
 CC is useful for evaluating structure and activity of a selected
 CC occupied and clustered transmembrane protein with the selected
 CC cytoplasmic domain and for identifying therapeutic compounds. It
 CC is also useful for identifying a cytoplasmic domain binding partner.
 CC It is may be used to study protein interactions with transmembrane
 CC proteins such as integrin, which can be used to treat conditions in
 CC which over activity of integrins is involved, such as inflammation,
 CC thrombosis and malignancy.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

Db 1 EILDV 5

Search completed: February 8, 2003, 10:29:08
 Job time : 33 secs

; CURRENT APPLICATION NUMBER: US/10/086,217

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:28:33 ; Search time 14 Seconds
(without alignments)
10.508 Million cell updates/sec

Title: US-09-251-073A-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	DB ID	Description	
1	23	100.0	5	1	US-08-109-106-3	Sequence 3, Appli
2	23	100.0	5	1	US-08-103-162A-3	Sequence 3, Appli
3	23	100.0	5	1	US-08-634-060-3	Sequence 3, Appli
4	23	100.0	5	1	US-08-338-282-10	Sequence 10, Appl
5	23	100.0	5	1	US-08-709-515-3	Sequence 3, Appli
6	23	100.0	5	2	US-08-700-846-2	Sequence 2, Appli
7	23	100.0	5	4	US-09-146-503-3	Sequence 2, Appli
8	23	100.0	5	4	US-08-983-391-2	Sequence 2, Appli
9	23	100.0	5	4	US-08-498-237-2	Sequence 2, Appli
10	23	100.0	5	4	US-08-376-372-2	Sequence 2, Appli
11	23	100.0	5	4	US-08-875-321-2	Sequence 2, Appli
12	23	100.0	5	5	PCT-US95-07542-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-109-106-3
; Sequence 3, Application US/08109106
; Patent No. 5475100
; GENERAL INFORMATION:
; APPLICANT: Kimikazu HASHINO et al.
; TITLE OF INVENTION: Artificial Antibody
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/109,106
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/725,668
FILING DATE: July 3, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-109-106-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 1 EILDV 5

RESULT 2
US-08-303-162A-3
; Sequence 3, Application US/08303162A
; Patent No. 5559099
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Brough, Douglas E.
; APPLICANT: Mcvey, Duncan L.
; APPLICANT: Brudey, Joseph T.
; TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
; TITLE OF INVENTION: AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,162A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr.
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 61306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-303-162A-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 1 EILDV 5

RESULT 3
US-08-634-060-3
; Sequence 3, Application US/08634060
; Patent No. 5712136
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelink, Petrus W.
; TITLE OF INVENTION: ADENOVIRAL-MEDIATED CELL TARGETING COMMANDED BY
; TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,060
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,162
; FILING DATE: 08-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr.
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 71602
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-634-060-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 1 EILDV 5

RESULT 4
US-08-338-282-10
; Sequence 10, Application US/08338282
; Patent No. 5730978
; GENERAL INFORMATION:
; APPLICANT: Wayter, E.A.
; TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,282
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/814,873
; FILING DATE: December 24, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/402,389

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; FILING DATE: September 1, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundemo, John S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: CYTE-1-6162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: EILDV
US-08-338-282-10

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 1 EILDV 5

RESULT 5
US-08-709-515-3
; Sequence 3, Application US/08709515
; Patent No. 573190
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Brough, Douglas B.
; APPLICANT: McVey, Douglas L.
; APPLICANT: Bruder, Joseph T.
; TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,515
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/303,162
; FILING DATE: 08-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr.
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 73845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5700
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 1 EILDV 5

RESULT 6
US-08-700-846-2
; Sequence 2, Application US/08700846
; Patent No. 5962311
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: ROSEVINK, PETRUS W.
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,846
; FILING DATE: 21-AUG-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: LARCHER, CAROL
; REGISTRATION NUMBER: 35243
; REFERENCE/DOCKET NUMBER: 74294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-700-846-2

Query Match 100.0%; Score 23; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 1 EILDV 5

RESULT 7
US-09-146-503-3
; Sequence 3, Application US/09146503
; Patent No. 6184206
; GENERAL INFORMATION:
; APPLICANT: Jeffrey W. Smith
; APPLICANT: Dana D. Hu
; TITLE OF INVENTION: Integrin Ligand Dissociators
; FILE REFERENCE: 02046.0002
; CURRENT APPLICATION NUMBER: US/09/146,503
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; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,463
; EARLIER FILING DATE: 1997-09-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-146-503-3

Query Match      100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 8
US-08-983-391-2
; Sequence 2, Application US/08983391
; Patent No. 6239108
; GENERAL INFORMATION:
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Adams, Steven P.
; APPLICANT: Castro, Alfredo C.
; APPLICANT: Zimmerman, Craig N.
; APPLICANT: Cuervo, Julio Herman
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Hammond, Charles E.
; APPLICANT: Carter, Mary Beth
; APPLICANT: Almquist, Ronald G.
; APPLICANT: Ensinger, Carol Lee
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; FILE REFERENCE: 10274/024002
; CURRENT APPLICATION NUMBER: US/08/983,391
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 96/11570
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: US 08/498,237
; PRIOR FILING DATE: 1995-07-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated protein
US-08-983-391-2

Query Match      100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 9
US-08-498-237-2
; Sequence 2, Application US/08498237
; Patent No. 6248713
; GENERAL INFORMATION:
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Adams, Steven P.
; APPLICANT: Castro, Alfredo C.
; APPLICANT: Zimmerman, Craig N
```

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; APPLICANT: Cuervo, Julio H
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Hammond, Charles E
; APPLICANT: Carter, Mary B
; APPLICANT: Almquist, Ronald G
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/498,237
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr. James P
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-08-498-237-2

Query Match      100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 10
US-08-376-372-2
; Sequence 2, Application US/08376372
; Patent No. 6306840
; GENERAL INFORMATION:
; APPLICANT: Adams, Steven P
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Castro, Alfredo C
; APPLICANT: Zimmerman, Craig N
; APPLICANT: Hammond, Charles E
; APPLICANT: Liao, Yu-Sheng
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-376-372-2

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 11

US-08-875-321-2
Sequence 2, Application US/08875321
Patent No. 6376538
GENERAL INFORMATION:
APPLICANT: Adams, Steven P.
APPLICANT: Lin, Ko-Chung
APPLICANT: Lee, Wen-Cherng
APPLICANT: Castro, Alfredo C.
APPLICANT: Zimmerman, Craig N.
APPLICANT: Hammond, Charles E.
APPLICANT: Liao, Yu-Sheng
APPLICANT: Cuervo, Julio Hernan
APPLICANT: Singh, Juswinder
TITLE OF INVENTION: CELL ADHESION INHIBITORS
FILE REFERENCE: 10274-023002
CURRENT APPLICATION NUMBER: US/08/875,321
CURRENT FILING DATE: 1997-09-27
PRIOR APPLICATION NUMBER: US 08/376, 372
PRIOR FILING DATE: 1995-01-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-2

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 12

PCT-US95-07542-3
Sequence 3, Application PC/TUS9507542
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS
NUMBER OF SEQUENCES: 20
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07542
FILING DATE: 13-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/260,514
FILING DATE: 15-JUN-1994
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Ligand sequence recognized by integrin
PCT-US95-07542-3

Query Match 100.0%; Score 23; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

Search completed: February 8, 2003, 10:30:42
Job time : 15 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:22:47 ; Search time 16 Seconds
(without alignments)
30.042 Million cell updates/sec

Title: US-09-251-073A-16

Perfect score: 23

Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 100 summaries

Database : PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	50	2 B86576	hypothetical prote
2	23	100.0	50	2 C72047	hypothetical prote
3	23	100.0	107	2 S13787	conserved hypotet
4	23	100.0	119	1 A69441	conserved hypotet
5	23	100.0	119	2 F84272	hypothetical prote
6	23	100.0	143	2 C44259	kinesin heavy chai
7	23	100.0	146	2 E90645	probable PTS enzym
8	23	100.0	146	2 E85496	probable PTS enzym
9	23	100.0	147	2 F70814	hypothetical prote
10	23	100.0	147	2 AG0772	probable exported
11	23	100.0	156	2 G82906	transcription elon
12	23	100.0	169	2 AH0568	phosphoribosylam
13	23	100.0	172	2 S24397	stellate protein -
14	23	100.0	172	2 S24398	stellate protein -
15	23	100.0	174	2 AF0390	shikimate kinase (
16	23	100.0	174	2 F97114	uncharacterized co
17	23	100.0	177	2 A64431	hypothetical prote
18	23	100.0	180	2 G95148	conserved hypotet
19	23	100.0	180	2 E98016	conserved hypotet
20	23	100.0	200	2 T48130	hypothetical prote
21	23	100.0	217	1 ZZZRRM	modulation protein
22	23	100.0	217	1 ZZZRRB4	modulation protein
23	23	100.0	217	2 B95321	NodB chitooligosac
24	23	100.0	222	2 C72400	conserved hypotet
25	23	100.0	231	2 B98297	hypothetical prote
26	23	100.0	231	2 AE2986	conserved hypotet
27	23	100.0	242	2 A69026	conserved hypotet
28	23	100.0	250	2 B91020	hypothetical prote
29	23	100.0	250	2 D85864	hypothetical prote

30	23	100.0	253	2 H70188	conserved hypotet
31	23	100.0	256	2 T32649	hypothetical prote
32	23	100.0	261	2 C55581	nasD protein - Kle
33	23	100.0	266	2 A95300	Nitrate transport
34	23	100.0	267	2 H90388	erythrocyte band 7
35	23	100.0	267	2 C64995	hypothetical prote
36	23	100.0	271	2 C86907	regulator of purin
37	23	100.0	286	2 S01402	H+-transporting tw
38	23	100.0	289	2 E97820	3-demethylubiquino
39	23	100.0	290	2 T21185	hypothetical prote
40	23	100.0	307	2 G81905	probable sulfate a
41	23	100.0	307	2 B81111	sulfate adenylyltr
42	23	100.0	307	2 S20383	phytoene synthase
43	23	100.0	312	2 T41157	probable 60s acidi
44	23	100.0	320	2 S73413	transcription anti
45	23	100.0	321	2 A95182	hypothetical prote
46	23	100.0	321	2 C89823	hypothetical prote
47	23	100.0	322	2 D98049	thioredoxin-disulf
48	23	100.0	322	2 T36941	probable transcrip
49	23	100.0	324	2 C71851	probable thiorodox
50	23	100.0	324	2 D64665	thioredoxin reduct
51	23	100.0	329	2 D69461	phosphoribosylform
52	23	100.0	332	2 S43988	protein phosphatas
53	23	100.0	333	2 A82377	conserved hypotet
54	23	100.0	337	2 AE2079	hypothetical prote
55	23	100.0	338	2 JC5436	aspartate-semialde
56	23	100.0	338	2 JC5435	aspartate-semialde
57	23	100.0	344	2 B70136	flagellar motor sw
58	23	100.0	351	2 S23508	dnaj protein homol
59	23	100.0	357	2 T41314	hypothetical repea
60	23	100.0	366	1 DJEC3B	DNA-directed DNA p
61	23	100.0	366	2 D91208	DNA polymerase III
62	23	100.0	366	2 F86054	DNA polymerase III
63	23	100.0	366	2 AB0958	DNA polymerase III
64	23	100.0	366	2 AF0497	DNA-directed DNA p
65	23	100.0	367	2 H97388	periplasmic mannit
66	23	100.0	367	2 A12606	hypothetical prote
67	23	100.0	380	1 S73751	high affinity tran
68	23	100.0	380	2 H69485	DNA-directed RNA p
69	23	100.0	380	2 B70076	aminoacylase homol
70	23	100.0	386	2 H72323	2-oxoglutarate-fer
71	23	100.0	402	1 E70302	molybdenum cofacto
72	23	100.0	403	2 T04821	hypothetical prote
73	23	100.0	407	2 E71087	hypothetical prote
74	23	100.0	408	2 S76678	hypothetical prote
75	23	100.0	414	1 Q9EC49	yafA protein, 49K
76	23	100.0	414	2 B90662	hypothetical prote
77	23	100.0	414	2 H85512	hypothetical prote
78	23	100.0	419	2 AD0543	conserved hypotet
79	23	100.0	419	2 T25577	hypothetical prote
80	23	100.0	435	2 E75001	hypothetical prote
81	23	100.0	442	2 A13252	thiophene and fura
82	23	100.0	457	2 C82311	hypothetical prote
83	23	100.0	466	2 H69065	5'-nucleotidase -
84	23	100.0	469	2 B81121	phage sheath prote
85	23	100.0	472	2 B56954	yes-associated pro
86	23	100.0	473	2 AC2251	hypothetical prote
87	23	100.0	484	2 A42065	ornithine decarbox
88	23	100.0	485	2 AB1342	transcription regu
89	23	100.0	486	2 I55449	gene PP2A protein
90	23	100.0	491	2 T23527	hypothetical prote
91	23	100.0	493	1 J70147	UMP synthase - fru
92	23	100.0	497	2 T28168	gene PP2A B protei
93	23	100.0	500	2 T28168	hypothetical prote
94	23	100.0	503	2 E98159	choline sulfatase
95	23	100.0	503	2 AD3128	choline sulfatase
96	23	100.0	508	2 T41345	probable allantoat
97	23	100.0	512	2 E64502	hypothetical prote
98	23	100.0	521	2 C75320	glycyl-tRNA synthe
99	23	100.0	535	2 T24309	hypothetical prote
100	23	100.0	551	2 H81552	methionyl-tRNA syn

RESULT 5

F84272
hypothetical protein Vng1169c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: F84272
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabcic Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: F84272
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <STO>
A;Cross-references: GB:AE004437; NID:g10580704; PIDN:AAG19546.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG1169C
C;Superfamily: conserved hypothetical protein MJ0039

Query Match 100.0%; Score 23; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
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Db 110 BILDV 114

RESULT 6

C44259
kinesin heavy chain homolog KIF5 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
C;Accession: C44259
R;Alzawa, H.; Sekine, Y.; Takemura, R.; Zhang, Z.; Nangaku, M.; Hirokawa, N.
J. Cell Biol. 119, 1287-1296, 1992
A;Title: Kinesin family in murine central nervous system.
A;Reference number: A44259; MUID:93077686; PMID:11447303
A;Accession: C44259
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-143 <AIZ>
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:118906)
C;Superfamily: kinesin heavy chain; kinesin motor domain homology
F;1-143/Domain: kinesin motor domain homology (fragment) <KMOT>

Query Match 100.0%; Score 23; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||
Db 91 BILDV 95

RESULT 7

E90645
probable PTS enzyme II B component [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: E90645
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90645

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA033556.1; PID:g13359589; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RMD 050952
C;Genetics:
A;Gene: EC60133

Query Match 100.0%; Score 23; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||
Db 15 BILDV 19

RESULT 8

E85496
probable PTS enzyme II B component [imported] - Escherichia coli (strain O157:H7, substr
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85496
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85496
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-146 <STO>
A;Cross-references: GB:AE005174; NID:g12512844; PIDN:AAG54433.1; GSPDB:GN00145; UWGP:201
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yadi

Query Match 100.0%; Score 23; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||
Db 15 BILDV 19

RESULT 9

F70814
hypothetical protein Rv0854 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: F70814
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70814
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-147 <COL>
A;Cross-references: GB:AL022004; GB:AL123456; NID:g3261550; PIDN:CAA17660.1; PID:g291691
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv0854
C;Superfamily: Streptomyces coelicolor hypothetical protein SC6G10.02c

Query Match 100.0%; Score 23; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 17 EILDV 21

RESULT 10

AG0772
C:Accession: AG0772
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A:Reference number: AB0502; PMID:11677608
A:Accession: AG0772
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-147 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02501.1; PID:g16503365; GSPDB:GN00176
C:Genetics:
A:Gene: STV2351

Query Match 100.0%; Score 23; DB 2; Length 147;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 98 EILDV 102

RESULT 11

G82906
Transcription elongation factor UU304 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: G82906
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: AB2870
A:Accession: G82906
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-156 <GIA>
A:Cross-references: GB:AE002128; GB:AF222894; NID:g6899279; PIDN:AAF30713.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: greA; UU304
A:Genetic code: SGC3
C:Superfamily: transcription elongation factor greB
C:Keywords: transcription factor

Query Match 100.0%; Score 23; DB 2; Length 156;

Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 20 EILDV 24

RESULT 12

AH0568
Phosphoribosylaminoimidazole carboxylase catalytic chain [imported] - Salmonella enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001

C:Accession: AH0568
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi
A:Reference number: AB0502; PMID:11677608
A:Accession: AH0568
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD05018.1; PID:g16501801; GSPDB:GN00176
C:Genetics:
A:Gene: STV0582
C:Superfamily: phosphoribosylaminoimidazole carboxylase catalytic chain; phosphoribosylaminoimidazole carboxylase catalytic chain

Query Match 100.0%; Score 23; DB 2; Length 169;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 31 EILDV 35

RESULT 13

S24397
Stellate protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Feb-1994 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C:Accession: S24397; S08120
R:Livak, K.J.
Genetics 124, 303-316, 1990
A:Title: Detailed structure of the Drosophila melanogaster Stellate genes and their trans
A:Reference number: S24397; MUID:90169476; PMID:1689686
A:Accession: S24397
A:Molecule type: DNA
A:Residues: 1-172 <LIV>
A:Cross-references: EMBL:X15899; NID:g8660; PIDN:CAA33906.1; PID:g295755
C:Genetics:
A:Gene: stellate
A:Cross-references: FlyBase:FBgn0003523
A:Introns: 4/2; 171/2

Query Match 100.0%; Score 23; DB 2; Length 172;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 46 EILDV 50

RESULT 14

S24398
Stellate protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C:Accession: S24398
R:Livak, K.J.
Genetics 124, 303-316, 1990
A:Title: Detailed structure of the Drosophila melanogaster Stellate genes and their tran
A:Reference number: S24397; MUID:90169476; PMID:1689686
A:Accession: S24398
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-172 <LIV>

Query Match 100.0%; Score 23; DB 2; Length 172;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 46 EILDV 50

RESULT 15

AF0390
shikimate kinase (EC 2.7.1.71) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 11-Jan-2002
C;Accession: AF0390
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC924450.1; PID:g15981151; GSPDB:GN00175
C;Genetics:
A;Gene: aroL
C;Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferase

Query Match 100.0%; Score 23; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 131 EILDV 135

RESULT 16

F97114
uncharacterized conserved protein (coiled-coil) CAC1739 [imported] - Clostridium acetobu
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C;Accession: F97114
R;Nolling, J.; Bretton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: F97114
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <KUR>
A;Cross-references: GB:AB001437; PIDN:AAK79705.1; PID:g15024707; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC1739

Query Match 100.0%; Score 23; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 32 EILDV 36

RESULT 17

A6431
hypothetical protein MJ1050 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: A6431
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.

rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A6431
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-177 <BUL>
A;Cross-references: GB:U67548; GB:L77117; NID:g2826361; PIDN:AB99053.1; PID:g1499895; T; C;Genetics:
C;Map position: FOR987440-987973
C;Superfamily: conserved hypothetical protein MJ1050

Query Match 100.0%; Score 23; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 118 EILDV 122

RESULT 18

G95148
conserved hypothetical protein SPI280 [imported] - Streptococcus pneumoniae (strain TIGR C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: G95148
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidnson, T.; Hickey, E.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, I. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95148
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75384.1; PID:g14972764; GSPDB:GN00164; TIGR:SP4 C;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SPI280

Query Match 100.0%; Score 23; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 33 EILDV 37

RESULT 19

E98016
conserved hypothetical protein spr1158 [imported] - Streptococcus pneumoniae (strain R6) C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: E98016
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Eyer, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Meyer, P.; Sun, P.M.; Winkler, M.E. J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: E98016
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAK99961.1; PID:g15458788; GSPDB:GN00174 C;Genetics:

A:Gene: spr1158

Query Match 100.0%; Score 23; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 33 EILDV 37

RESULT 20

T48130

hypothetical protein T4C9.40 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C:Accession: T48130

R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dickse, W.; Stiekema, W.; Bancroft, I.; Mew

submitted to the Protein Sequence Database, June 1999

A:Reference number: 224485

A:Accession: T48130

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-200 <BEV>

A:Cross-references: EMBL:AL080318

A:Experimental source: EMBL:AL080318; BAC clone T4C9

C:Genetics:

A:Map position: 4

A:Introns: 132/1

A:Note: T4C9.40

Query Match 100.0%; Score 23; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 66 EILDV 70

RESULT 21

ZZZRBM

modulation protein nodB - Rhizobium meliloti

C:Species: Rhizobium meliloti

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 11-Apr-1997

C:Accession: A03483

R:Engelhoff, T.T.; Fisher, R.F.; Jacobs, T.W.; Mulligan, J.T.; Long, S.R.

DNA 4, 241-248, 1985

A:Title: Nucleotide sequence of Rhizobium meliloti 1021 nodulation genes: nodB is read

A:Reference number: A90951; MUID:85223955; PMID:4006668

A:Accession: A03483

A:Molecule type: DNA

A:Residues: 1-217 <EGE>

A:Cross-references: GB:X01649

A:Experimental source: strain 1021 symbiotic plasmid

C:Comment: This is one of the proteins, coded by nodulation genes, that are required for

C:Genetics:

A:Gene: nodB

C:Superfamily: nodulation protein nodB; nodB homology

C:Keywords: nodulation

F:26-175/Domain: nodB homology <NODB>

Query Match 100.0%; Score 23; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 38 EILDV 42

RESULT 22

ZZZRB4

conserved hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

modulation protein nodB - Rhizobium meliloti (strain 41)

C:Species: Rhizobium meliloti

C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999

C:Accession: A03484

R:Torok, I.; Kondorosi, E.; Stepkowski, T.; Posfai, J.; Kondorosi, A.

Nucleic Acids Res. 12, 9509-9524, 1984

A:Title: Nucleotide sequence of Rhizobium meliloti nodulation genes.

A:Reference number: A93553; MUID:85087953; PMID:6336331

A:Accession: A03484

A:Molecule type: DNA

A:Residues: 1-217 <TOR>

A:Cross-references: GB:X01649; GB:M13287; NID:g46287; PIDN:CAA25809.1; PID:g46290

A:Experimental source: strain 41

C:Comment: This is one of the proteins, coded by nodulation genes, that are required for

C:Genetics:

A:Gene: nodB

C:Superfamily: nodulation protein nodB; nodB homology

C:Keywords: nodulation

F:26-175/Domain: nodB homology <NODB>

Query Match 100.0%; Score 23; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 38 EILDV 42

RESULT 23

B95321

NodB chitooligosaccharide deacetylase [imported] - Sinorhizobium meliloti (strain 1021)

C:Species: Sinorhizobium meliloti

C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: B95321

R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9886, 2001

A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A:Reference number: A95262; MUID:21396509; PMID:11481432

A:Accession: B95321

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-217 <KUR>

A:Cross-references: GB:AE006469; PIDN:AAK65132.1; PID:g14523571; GSPDB:GN00165

A:Experimental source: strain 1021, megaplasmid pSymA

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: nodB

A:Genome: plasmid

C:Superfamily: nodulation protein nodB; nodB homology

Query Match 100.0%; Score 23; DB 2; Length 217;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 38 EILDV 42

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C;Accession: C72400
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:9287316; PMID:10360571
 A;Accession: C72400
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-222 <ARN>
 A;Cross-references: GB:AE001708; GB:AE000512; MID:g4980740; PIDN:AAD35348.1; PID:g498075
 A;Experimental source: strain MSB8
 C;Genetics:
 A;Gene: TM0260

Query Match 100.0%; Score 23; DB 2; Length 222;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||
 Db 91 EILDV 95

RESULT 25
 B98297
 hypothetical protein AGR_L_2665 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C;Species: Agrobacterium tumefaciens
 C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
 C;Accession: B98297
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quresh, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A;Reference number: A97359; PMID:11743194
 A;Accession: B98297
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-231 <KUR>
 A;Cross-references: GB:AE007870; PIDN:AAK89900.1; PID:g15159849; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L_2665
 A;Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||
 Db 2 EILDV 6

RESULT 26
 AE2386
 conserved hypothetical protein Atu3494 [imported] - Agrobacterium tumefaciens (strain C5
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C;Accession: AE2386
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:11743193
 A;Accession: AE2386
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-231 <KUR>

A;Cross-references: GB:AE008689; PIDN:AAI44307.1; PID:g17741896; GSPDB:GN00187
 A;Experimental source: strain CS8 (Dupont)
 C;Genetics:
 A;Gene: Atu3494
 A;Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||
 Db 2 EILDV 6

RESULT 27
 A69026
 conserved hypothetical protein MTH1192 - Methanobacterium thermoautotrophicum (strain Del
 C;Species: Methanobacterium thermoautotrophicum
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C;Accession: A69026
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I
 ; Liu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwanli, N.;
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
 A;Reference number: A69000; MUID:98037514; PMID:9371463
 A;Accession: A69026
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-242 <MTH>
 A;Cross-references: GB:AE000887; GB:AE000666; MID:g2622289; PIDN:AA885681.1; PID:g262230
 A;Experimental source: strain Delta H
 C;Genetics:
 A;Gene: MTH1192
 A;Start codon: GTG

Query Match 100.0%; Score 23; DB 2; Length 242;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||
 Db 174 EILDV 178

RESULT 28
 B91020
 hypothetical protein Ec3130 [imported] - Escherichia coli (strain O157:H7, substrain RN
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C;Accession: B91020
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: B91020
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-250 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA836553.1; PID:g13362600; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: Ec3130
 C;Superfamily: 2,4-dihydroxyhept-2-ene-1,7

Query Match 100.0%; Score 23; DB 2; Length 250;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 |||||

Db 146 EILDV 150

RESULT 29
D85864
hypothetical protein Z3503 [imported] - Escherichia coli (strain O157:H7, substrain EDL958)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: D85864
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85864
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <STO>
A:Cross-references: GB:AF005174; NID:gl2516598; PIDN:AA657376.1; GSPDB:GN00145; UWGP:Z35
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z3503
C:Superfamily: 2,4-dihydroxyhept-2-ene-1,7

Query Match 100.0%; Score 23; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 146 EILDV 150

RESULT 30
H70188
conserved hypothetical protein BB0713 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: H70188
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, S.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70188
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-253 <KLE>
A:Cross-references: GB:AF001171; GB:AE000783; NID:G2688640; PIDN:AA67060.1; PID:G268864
A:Experimental source: strain B31

Query Match 100.0%; Score 23; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 125 EILDV 129

RESULT 31
T32649
hypothetical protein H10D12.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32649
R:Ozersky, P.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid H10D12.
A:Reference number: Z21205
A:Accession: T32649

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-256 <OZE>
A:Cross-references: EMBL:AF038620; PIDN:AA93487.1; GSPDB:GN00022; CESP:H10D12.2
A:Experimental source: strain Bristol N2; clone H10D12
C:Genetics:
A:Gene: CESP:H10D12.2
A:Map position: 4
A:Introns: 25/1; 80/1; 133/1

Query Match 100.0%; Score 23; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 75 EILDV 79

RESULT 32
C55581
nasD protein - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C>Date: 25-Aug-1995 #sequence_revision 25-Aug-1995 #text_change 02-Feb-2001
C:Accession: C55581
R:Lin, J.T.; Goldman, B.S.; Stewart, V.
J. Bacteriol. 176, 2551-2559, 1994
A:Title: The nasFEDCBA operon for nitrate and nitrite assimilation in Klebsiella pneumoniae
A:Reference number: A55581; MUID:94222832; PMID:8169203
A:Accession: C55581
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-261 <LIN>
A:Cross-references: GB:L27431; NID:gl119218; PID:G473439
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:23-214/Domain: ATP-binding cassette homology <ABC>
F:40-47/Region: nucleotide-binding motif A (P-loop)

Query Match 100.0%; Score 23; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 221 EILDV 225

RESULT 33
A95300
Nitrate transport ATP binding protein, probable Sma0581 [imported] - Sinorhizobium meliloti
C:Species: Sinorhizobium meliloti
C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 17-May-2002
C:Accession: A95300
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bower
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A:Reference number: A95262; MUID:21396509; PMID:11481432
A:Accession: A95300
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <KUR>
A:Cross-references: GB:AE006469; PIDN:AAK4963.1; PID:gl4523388; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.;
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation
C;Genetics:
A;Gene: Sma0581
A;Genome: plasmid
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology

Query Match 100.0%; Score 23; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 223 EILDV 227

RESULT 34

H90388
erythrocyte band 7 membrane protein homolog [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: H90388
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: H90388

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-267 <KUR>

A;Cross-references: GB:AE006641; NID:g13815493; PIDN:AAK42367.1; GSPDB:GN00155

C;Genetics:

A;Gene: SS02195

C;Superfamily: erythrocyte band 7 integral membrane protein

Query Match 100.0%; Score 23; DB 2; Length 267;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 146 EILDV 150

RESULT 35

C64995
hypothetical protein b2245 - Escherichia coli (strain K-12)

C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: C64995
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: C64995

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-267 <BLAT>

A;Cross-references: GB:AE000314; GB:U00096; NID:g1788570; PIDN:AAC75305.1; PID:g1788578;
A;Experimental source: strain K-12, substrain MG1655

C;Superfamily: 2,4-dihydroxyhept-2-ene-1,7

Query Match 100.0%; Score 23; DB 2; Length 267;

Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 163 EILDV 167

RESULT 36

C86907

regulator of purine biosynthetic genes [imported] - Lactococcus lactis subsp. lactis (str;
C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C;Accession: C86907

R;Bolotin, A.; Mincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: C86907

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-271 <STO>

A;Cross-references: GB:AE005176; PID:g12725330; PIDN:AAK06357.1; GSPDB:GN00146

A;Experimental source: strain IL1403

C;Genetics:

A;Gene: purR

Query Match 100.0%; Score 23; DB 2; Length 271;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 148 EILDV 152

RESULT 37

S01402

H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - thermophilic bacterium PS-;
C;Species: thermophilic bacterium PS-3

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Jun-2002

C;Accession: S01402

R;Ohta, S.; Yohda, M.; Ishizuka, M.; Hirata, H.; Hamamoto, T.; Otawara-Hamamoto, Y.; Mat

Biochim. Biophys. Acta 933, 141-155, 1988

A;Title: Sequence and over-expression of subunits of adenosine triphosphate synthase in

A;Reference number: S01397; MUID:88163679; PMID:2894854

A;Accession: S01402

A;Molecule type: DNA

A;Residues: 1-286 <OHT>

A;Cross-references: EMBL:X07804; NID:g45808; PIDN:CAA30653.1; PID:g581474

A;Note: part of this sequence, including the amino end of the mature protein, was confin

C;Genetics:

A;Start codon: GTG

C;Superfamily: H+-transporting ATP synthase gamma chain

C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

F;5-286/Product: H+-transporting ATP synthase gamma chain #status experimental <MAT>

Query Match 100.0%; Score 23; DB 2; Length 286;

Best Local Similarity 100.0%; Pred. No. 4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 212 EILDV 216

RESULT 38

E97820

3-demethylubiquinone-9 3-methyltransferase [imported] - Rickettsia conorii (strain Malles)

C;Species: Rickettsia conorii

C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 01-Mar-2002

C;Accession: E97820

R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

Science 293, 2093-2098, 2001

A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A;Reference number: A97700; MUID:21442074; PMID:11557893

A;Accession: E97820

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-289 <KUR>

A;Cross-references: GB:AE006914; PIDN:AAL03503.1; PID:g15620077; GSPDB:GN00173

C;Genetics:
A;Gene: ubiG
C;Superfamily: 3-demethylubiquinone-9-3-O-methyltransferase; bioC homology

Query Match 100.0%; Score 23; DB 2; Length 289;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BILDV 5
|
|
|
|
DB 104 EILDV 108

RESULT 39
T21185
hypothetical protein F21A3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C;Accession: T21185
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19387
A;Accession: T21185
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-290 <WIL>
A;Cross-references: EMBL:Z81509; PIDN:CA304157.1; GSPDB:GN00023; CESP:F21A3.3
A;Experimental source: clone F21A3
C;Genetics:
A;Gene: CESP:F21A3.3
A;Map position: 5
A;Introns: 26/1; 66/1; 111/1; 139/2; 170/2; 221/1
C;Superfamily: Caenorhabditis elegans hypothetical protein ZC13.4

Query Match 100.0%; Score 23; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BILDV 5
|
|
|
|
DB 150 EILDV 154

RESULT 40
G81905
probable sulfate adenylyltransferase (EC 2.7.7.4) chain 2 NMA1365 [imported] - Neisseria
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: G81905
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-307 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CA884611.1; PID:g738003
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: cyrD; NMA1365
C;Superfamily: nodulation protein nodP
C;Keywords: nucleotidyltransferase

Query Match 100.0%; Score 23; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BILDV 5
|
|
|
|
DB 244 EILDV 248

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000

C/Accession: T41157

R/Hilbert, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, October 1998

A:Reference number: 221973

A/Accession: T41157

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-312 <Hil>

A/Cross-references: EMBL:AL031907; PIDN:CAA21428.1; GSPDB:GN00068; SPDB:SPCC18.14c

A:Experimental source: strain 972h-; cosmid c18

C/Genetics:

A:Gene: SPDB:SPCC18.14c

A/Map position: 3

A/Introns: 262/3

C/Superfamily: rat acidic ribosomal protein P0

Query Match 100.0%; Score 23; DB 2; Length 312;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 200 EILDV 204

RESULT 44

S73413

N/Transcription antitermination factor nusG - Mycoplasma pneumoniae (strain ATCC 29342)

A/Alternate names: hypothetical protein D09_orf320

C/Species: Mycoplasma pneumoniae

A/Variety: ATCC 29342

C/Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999

C/Accession: S73413

R/Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.

Nucleic Acids Res. 24, 4420-4449, 1996

A/Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A/Reference number: S73327; MUID:97105885; PMID:8948633

A/Accession: S73413

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-320 <HM>

A/Cross-references: EMBL:AE000011; GB:U00089; NID:g1673740; PIDN:AAB95735.1; PID:g167374

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C/Genetics:

A:Gene: nusG

A:Genetic code: SGC3

Query Match 100.0%; Score 23; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 38 EILDV 42

RESULT 45

A95182

H/hypothetical protein SPI563 [imported] - Streptococcus pneumoniae (strain TIGR4)

C/Species: Streptococcus pneumoniae

C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 01-Feb-2002

C/Accession: A95182

R/Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Hickey, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Umayam, E.K.; Holt, I.E.
Science 293, 498-506, 2001

A/Authors: Lofus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A/Reference number: A95000; MUID:21357209; PMID:11463916

A/Accession: A95182

A/Status: preliminary

A/Molecule type: DNA

A;Residues: 1-321 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75650.1; PID:g14973054; GSPDB:GN00164; TIGR:SP4;
A;Experimental source: strain TIGR4
C:Genetics:
A;Gene: SPI563
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology

Query Match 100.0%; Score 23; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||
Db 51 BILDV 55

RESULT 46
C89823
Hypothetical protein SA0511 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89823
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89823
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-321 <KUR>
A;Cross-references: GB:BA000018; PID:g13700444; PIDN:BA841742.1; GSPDB:GN00149
A;Experimental source: strain N315
C:Genetics:
A;Gene: SA0511

Query Match 100.0%; Score 23; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||
Db 50 BILDV 54

RESULT 47
D98049
thioredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae (strai
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
C:Accession: D98049
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; Br
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
J. P.; Sun, P.M.; Winkler, M.E.
Y. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D98049
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-322 <KUR>
A;Cross-references: GB:AE007317; PIDN:AAL00225.1; PID:g15459075; GSPDB:GN00174
C:Genetics:
A;Gene: trxB
C;Superfamily: thioredoxin reductase; thioredoxin reductase homology
C;Keywords: oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 51 EILDV 55

RESULT 48
T36941
probable transcription initiation factor sigma - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T36941
R;Seeger, K.J.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.;
submitted to the EMBL Data Library, September 1999
A;Reference number: 221607
A;Accession: T36941
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-322 <SEE>
A;Cross-references: EMBL:AL109962; PIDN:CAB53126.1; GSPDB:GN00070; SCORDB:SCJ1.08
C;Genetics:
C;Gene: SCORDB:SCJ1.08
C;Keywords: transcription initiation

Query Match 100.0%; Score 23; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 148 EILDV 152

RESULT 49
C71851
probable thioredoxin reductase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C;Accession: C71851
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:95120557; PMID:9923682
A;Accession: C71851
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <ARN>
A;Cross-references: GB:AE001536; GB:AE001439; NID:94155675; PIDN:AAD06662.1; PID:G415567
C;Genetics:
A;Gene: trxB_2

Query Match 100.0%; Score 23; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 4 EILDV 8

RESULT 50
D64665
thioredoxin reductase - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: D64665
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: D64665
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-324 <TOM>
A;Cross-references: GB:AE000622; GB:AE000511; NID:G2314317; PIDN:AAD08209.1; PID:G2314321

Query Match 100.0%; Score 23; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 4 EILDV 8

RESULT 51
D69461
phosphoribosylformylglycinamide cyclo-ligase (purM) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
C;Accession: D69461
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uitterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69461
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-329 <KLE>
A;Cross-references: GB:AE000986; GB:AE000782; NID:G2689309; PIDN:AA889555.1; PID:G2648860
C;Superfamily: phosphoribosylformylglycinamide cyclo-ligase; phosphoribosylformylglyci
F;6-326/Domain: phosphoribosylformylglycinamide cyclo-ligase homology <PFCU>

Query Match 100.0%; Score 23; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 222 EILDV 226

RESULT 52
S43988
protein phosphatases pp1 regulatory subunit sds22 - fission yeast (Schizosaccharomyces po
C;Species: Schizosaccharomyces pombe
C;Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 26-May-2000
C;Accession: S43988; T38782; A38439
R;Stone, E.M.; Yamano, H.; Kinoshita, N.; Yanagida, M.
Curr. Biol. 3, 13-26, 1993
A;Title: Mitotic regulation of protein phosphatases by the fission yeast sds22 protein.
A;Reference number: S43988
A;Accession: S43988
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-332 <STO>
R;Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z21751
A;Accession: T38782
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-332 <SKS>
A;Cross-references: EMBL:Z98762; PIDN:CAB11482.1; GSPDB:GN00066; SPDB:SPAC4A8.12C
A;Experimental source: strain 972h-; cosmid c4A8
R;Ohkura, H.; Yanagida, M.

Cell 64, 149-157, 1991
A;Title: Schizosaccharomyces pombe sds22+ essential for a midmitotic transition end
A;Reference number: A38439; MUID:91098642; PMID:1846086
A;Accession: A38439
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 53-332 <CHK>
A;Cross-references: GB:M57495; NID:g173478; PIDN:AAA35342.1; PID:g173479
C;Genetics:
A;Gene: sds22; SPAC4A8.12c
A;Map position: 1
A;Introns: 41/3
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan
C;Keywords: nucleus

Query Match 100.0%; Score 23; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 240 EILDV 244

RESULT 53
A82937
conserved hypothetical UU077 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: A82937
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: A82937
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-333 <GLA>
A;Cross-references: GB:AF002107; GB:AF222894; NID:96899022; PIDN:AAF30482.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: UU077
A;Genetic code: SGC3

Query Match 100.0%; Score 23; DB 2; Length 333;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 74 EILDV 78

RESULT 54
AE2079
hypothetical protein alr2187 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AE2079
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-337 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB73886.1; PID:g17131278; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr2187

Query Match 100.0%; Score 23; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 212 EILDV 216

RESULT 55

JC5436

aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - Shewanella sp. DSS12
N;Alternate names: aspartate beta-D-semialdehyde dehydrogenase
C;Species: Shewanella sp. DSS12

C;Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C;Accession: JC5436

R;Kato, C.; Smorawinska, M.; Li, L.; Horikoshi, K.

J. Biochem. 121, 717-723, 1997

A;Title: Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenase

A;Reference number: JC5435; MUID:97306055; PMID:9163523

A;Accession: JC5436

A;Molecule type: DNA

A;Residues: 1-338 <KAT>

A;Cross-references: DDBJ:D49540; NID:g747690; PIDN:BAA08490.1; PID:g747692

A;Experimental source: strain DSS12

C;Comment: This enzyme is a key enzyme in the biosynthetic pathway of lysine, threonine,

C;Genetics:

A;Gene: asd

C;Superfamily: aspartate-semialdehyde dehydrogenase

C;Keywords: oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

|

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|

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Db 55 EILDV 59

RESULT 56

JC5435

aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - Shewanella sp. DB6705

N;Alternate names: aspartate beta-D-semialdehyde dehydrogenase

C;Species: Shewanella sp. DB6705

C;Date: 17-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 20-Jun-2000

C;Accession: JC5435

R;Kato, C.; Smorawinska, M.; Li, L.; Horikoshi, K.

J. Biochem. 121, 717-723, 1997

A;Title: Comparison of the gene expression of aspartate beta-D-semialdehyde dehydrogenase

A;Reference number: JC5435; MUID:97306055; PMID:9163523

A;Accession: JC5435

A;Molecule type: DNA

A;Residues: 1-338 <KAT>

A;Cross-references: DDBJ:D49539; NID:g747687; PIDN:BAA08488.1; PID:g747689

A;Experimental source: strain DB6705

C;Comment: This enzyme is a key enzyme in the biosynthetic pathway of lysine, threonine,

C;Genetics:

A;Gene: asd

C;Superfamily: aspartate-semialdehyde dehydrogenase

C;Keywords: oxidoreductase

Query Match 100.0%; Score 23; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

|

|

|

|

Db 55 EILDV 59

RESULT 57

B70136
flagellar motor switch protein (fliG-2) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 26-Aug-1999
C:Accession: B70136
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Karlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: B70136
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-344 <KLE>
A:Cross-references: GB:AE001137; GB:AE000783; NID:G2689160; PIDN:AAC66658.1; PID:G268817
A:Experimental source: strain B31
C:Superfamily: flagellar switch protein fliG

Query Match 100.0%; Score 23; DB 2; Length 344;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 8 EILDV 12

RESULT 58
S23508
dnaJ protein homolog - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
C:Accession: S23508; S23509
R:Cheetham, M.B.; Brion, J.P.; Anderton, B.H.
Biochem. J. 284, 469-476, 1992
A:Title: Human homologues of the bacterial heat-shock protein DnaJ are preferentially ex
A:Reference number: S23508; MUID:92287055; PMID:1599432
A:Accession: S23508
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-351 <CHE>
A:Cross-references: EMBL:X63368; NID:G32468; PIDN:CAA44968.1; PID:G32469
A:Accession: S23509
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-274, 'DVF', <CH2>
A:Cross-references: EMBL:X63368; NID:G32468; PIDN:CAA44969.1; PID:G32470
C:Genetics:
A:Introns: 275/1
C:Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;3-69/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 100.0%; Score 23; DB 2; Length 351;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 6 EILDV 10

RESULT 59
T41314
hypothetical repeat-containing protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T41314
R:William, R.; Barrell, B.G.; Rajandream, M.A.; Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21987
A:Accession: T41314

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-357 <GWI>
A:Cross-references: EMBL:AL031603; PIDN:CAA20909.1; GSPDB:GN000668; SPDB:SPCC330.04c
A:Experimental source: strain 972h-; cosmid c330
C:Genetics:
A:Gene: SPDB:SPCC330.04c
A:Map position: 3

Query Match 100.0%; Score 23; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 238 EILDV 242

RESULT 60
DJEC3B
DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 28-Aug-1985 #sequence_revision 31-Mar-1988 #text_change 01-Mar-2002
C:Accession: A91510; A93996; A22168; I41190; I54000; F65172; A00719; B24944
R:Ohmori, H.; Kimura, M.; Nagata, T.; Sakakibara, Y.
Gene 28, 159-170, 1984
A:Title: Structural analysis of the dnaA and dnaN genes of Escherichia coli.
A:Reference number: A91510; MUID:84237568; PMID:6234204
A:Accession: A91510
A:Molecule type: DNA
A:Residues: 1-366 <OHM>
A:Cross-references: GB:J01602; NID:G145758; PIDN:AAB59150.1; PID:G145761
A:Experimental source: strain K-12
R:Blanc, M.A.; Sandler, S.J.; Armengod, M.B.; Ream, L.W.; Clark, A.J.
Proc. Natl. Acad. Sci. U.S.A. 81, 4622-4626, 1984
A:Title: Molecular analysis of the recF gene of Escherichia coli.
A:Reference number: A93996; MUID:84272685; PMID:6379647
A:Accession: A93996
A:Molecule type: DNA
A:Residues: 297-366 <BLA>
A:Cross-references: GB:K02179; NID:G147537; PIDN:AAA24510.1; PID:G147538
R:Adachi, T.; Mizuuchi, K.; Menzel, R.; Gellert, M.
Nucleic Acids Res. 12, 6389-6395, 1984
A:Title: DNA sequence and transcription of the region upstream of the E. coli gyrB gene.
A:Reference number: A22168; MUID:84297235; PMID:6089112
A:Accession: A22168
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 342-366 <ADA>
A:Cross-references: GB:X04341; GB:X00870; NID:G41643; PIDN:CAA27869.1; PID:G41644
A:Experimental source: strain K-12
R:Armengod, M.
J. Biol. Chem. 263, 12109-12114, 1988
A:Title: Transcriptional organization of the dnaN and recF genes of Escherichia coli K-12
A:Reference number: I41190; MUID:88298898; PMID:2841344
A:Accession: I41190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <RES>
A:Cross-references: GB:M19876; NID:G145779; PIDN:AAA23695.1; PID:G551800
R:Armengod, M.
Gene 43, 183-196, 1986
A:Title: Overlapping arrangement of the recF and dnaN operons of Escherichia coli; Positi
A:Reference number: I54000; MUID:86301872; PMID:3527871
A:Accession: I54000
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 143-170 <RE2>
A:Cross-references: GB:M13822; NID:G147541; PIDN:AAA24512.1; PID:G147542
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65172
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-366 <BLAT>
A;Cross-references: GB:AE000447; GB:U00096; NID:G2367266; PIDN:AAC76724.1; PID:gl790136;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: dnaN
A;Map position: 83 min
A;Complex: DNA polymerase III is a multichain complex; alpha, epsilon, theta, tau, gamma
C;Function: <GEN>
A;Description: DNA synthesis; synthesizes both, the lagging and the leading strands in E
A;Pathway: DNA biosynthesis
A;Note: core enzyme (catalytic core) contains alpha, epsilon and theta; alpha cha
required for assembly; tau allows dimerization of the core complex and processivity is
te; the holoenzyme is completed by addition of beta chain which clamps the enzyme to DNA
C;Function: <BPT>
A;Description: beta chain is required for initiation of replication
A;Note: can slide along duplex DNA bidirectionally and ATP-independent; binds core; crys
C;Superfamily: DNA-directed DNA polymerase III beta chain
C;Keywords: DNA replication initiation; nucleotidyltransferase

Query Match 100.0%; Score 23; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 304 EILDV 308

RESULT 61
D91208
DNA polymerase III beta-subunit [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: D91208
R;Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91208
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA838059.1; PID:gl3364111; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs4636
C;Superfamily: DNA-directed DNA polymerase III beta chain

Query Match 100.0%; Score 23; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 304 EILDV 308

RESULT 62
F86054
DNA polymerase III, beta-subunit [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F86054
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: F86054
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <STO>
A;Cross-references: GB:AE005174; NID:gl2518540; PIDN:AAG58898.1; GSPDB:GN00145; UWGP:251;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: dnaN
C;Superfamily: DNA-directed DNA polymerase III beta chain

Query Match 100.0%; Score 23; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 304 EILDV 308

RESULT 63
AB0958
DNA polymerase III beta-chain [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB0958
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AB0958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03158.1; PID:gl6504793; GSPDB:GN00176
C;Genetics:
A;Gene: STV3941
C;Superfamily: DNA-directed DNA polymerase III beta chain

Query Match 100.0%; Score 23; DB 2; Length 366;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 304 EILDV 308

RESULT 64
AF0497
DNA-directed DNA polymerase (EC 2.7.7.7) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AF0497
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, i
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0497
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93546.1; PID:gl5981986; GSPDB:GN00175
C;Genetics:
A;Gene: dnaN
C;Superfamily: DNA-directed DNA polymerase III beta chain
C;Keywords: nucleotidyltransferase

Query Match 100.0%; Score 23; DB 2; Length 366;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 304 EILDV 308
 |||||

RESULT 65
 H97388
 periplasmic mannitol-binding protein, smom (AF018073) [imported] - Agrobacterium tumefaciens
 C;Species: Agrobacterium tumefaciens
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C;Accession: H97388
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A;Reference number: A97359; PMID:11743194
 A;Accession: H97388
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-367 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK86065.1; PID:gl5155140; GSPDB:GN00169
 C;Genetics:
 A;Gene: AGR_C_426
 A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 367;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 306 EILDV 310
 |||||

RESULT 66
 A12606
 hypothetical protein Atu0249 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C;Accession: A12606
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2577; PMID:11743193
 A;Accession: A12606
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-367 <KUR>
 A;Cross-references: GB:AE008688; PIDN:AAI41271.1; PID:gl7738578; GSPDB:GN00186
 C;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu0249
 A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 367;
 Best Local Similarity 100.0%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 306 EILDV 310
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RESULT 67
 S73751

high affinity transport system protein P37 - Mycoplasma pneumoniae (strain ATCC 29342)
 N;Alternate names: hypothetical protein A05_orf380V
 C;Species: Mycoplasma pneumoniae
 A;Variety: ATCC 29342
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999
 C;Accession: S73751
 R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
 A;Reference number: S73327; MUID:97105885; PMID:8948633
 A;Accession: S73751
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-380 <HIM>
 A;Cross-references: EMBL:AE000041; GB:U00089; NID:gl674104; PIDN:AB96073.1; PID:gl674111
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C;Genetics:
 A;Gene: P37
 A;Genetic code: SGC3
 A;Start codon: GTG
 C;Superfamily: Mycoplasma hyorhinis high affinity transport system protein P37

Query Match 100.0%; Score 23; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 370 EILDV 374
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RESULT 68
 H69485
 DNA-directed RNA polymerase, subunit A'' (rpoA2) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 18-Jun-1999
 C;Accession: H69485
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.P.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.M.; Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: H69485
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-380 <KLE>
 A;Cross-references: GB:AE000972; GB:AE000782; NID:g2689295; PIDN:AB89364.1; PID:g264885;
 C;Superfamily: DNA-directed RNA polymerase II

Query Match 100.0%; Score 23; DB 2; Length 380;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 98 EILDV 102
 |||||

RESULT 69
 B70076
 aminoacylase homolog yxeP - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C;Accession: B70076
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chon
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erttington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallero
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serod akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B70076
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:G2636442; PIDN:CAB15983.1; PID:G2636493
A;Experimental source: strain 168
C;Genetics:
A;Gene: vxep
C;Superfamily: hippurate hydrolase

Query Match 100.0%; Score 23; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 44 EILDV 48
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RESULT 70
H72323
2-oxoglutarate-ferredoxin oxidoreductase (EC 1.2.7.-) alpha chain TM0878 [similarity] -
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72323
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: H72323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <ARN>
A;Cross-references: GB:AE001753; GB:AE000512; NID:94981397; PIDN:AAD35959.1; PID:G498141
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0878
C;Superfamily: Helicobacter pylori 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid ferred
C;Keywords: oxidoreductase
P;8-189/Domain: 2-oxoacid ferredoxin oxidoreductase homology <P80>

Query Match 100.0%; Score 23; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 374 EILDV 378
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RESULT 71
E70302
molybdenum cofactor biosynthesis protein A - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: E70302
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: E70302
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-402 <AQF>
A;Cross-references: GB:AE000657; GB:AE000657; NID:G2982779; PIDN:AAC06407.1; PID:G298278;
A;Experimental source: strain VF5
C;Genetics:
A;Gene: moeA1
C;Superfamily: molybdenum cofactor biosynthesis protein moeA-2

Query Match 100.0%; Score 23; DB 1; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 185 EILDV 189
|||||

RESULT 72
T04821
hypothetical protein F10M23.320 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 04-Mar-2000
C;Accession: T04821
R;Bevan, M.; Lecharny, A.; Chedford, F.; Krivitzky, M.; Kreis, M.; Hoheisel, J.; Mewes, H.
submitted to the Protein Sequence Database, February 1999

A;Reference number: Z15385
A;Accession: T04821
A;Molecule type: DNA
A;Residues: 1-403 <BEV>
A;Cross-references: EMBL:AL035440
A;Experimental source: cultivar Columbia; BAC clone F10M23
C;Genetics:
A;Map position: 4
A;Introns: 68/1; 110/3; 176/2; 195/2; 221/2; 269/3
A;Note: F10M23.320
C;Superfamily: Arabidopsis thaliana hypothetical protein F10M23.320

Query Match 100.0%; Score 23; DB 2; Length 403;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 137 EILDV 141
|||||

RESULT 73
E71087
hypothetical protein PH0962 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: E71087
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: E71087
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-407 <KAW>
A;Cross-references: GB:AP000004; NID:G3236131; PIDN:BAA30059.1; PID:G3257376
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH0962
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0041

Query Match 100.0%; Score 23; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 8, 2003, 10:25:02
Job time : 21 secs

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Qy      1 EILDV 5
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Db     389 EILDV 393

RESULT 74
S76678
hypotheical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76678
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76678
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-408 <KAN>
A:Cross-references: EMBL:D64004; GB:AB001339; NID:g1001701; PIDN:BAA10622.1; PID:g120845
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      100.0%; Score 23; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EILDV 5
      |||||
Db     378 EILDV 382

RESULT 75
QOEC49
yafA protein, 49K - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 04-Dec-1986 #sequence_revision 05-Dec-1997 #text_change 01-Mar-2002
C:Accession: H64748; A04451
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64748
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-414 <BLAT>
A:Cross-references: GB:AE000132; GB:U00096; NID:g2367098; PIDN:AACT3343.1; PID:g1786434;
A:Experimental source: strain K-12, substrain MG1655
R:Nuesch, J.; Schumperli, D.
Gene 32, 243-249, 1984
A:Title: Structural and functional organization of the gpt gene region of Escherichia co
A:Reference number: A91517; MUID:85155481; PMID:6397401
A:Accession: A04451
A:Molecule type: DNA
A:Residues: 1-241,'S',243-276,'TL',279-396,'KILTKVFRKSPGTS',411,'NA',414,'VKNLLNFAFLVKQI
A:Cross-references: GB:M13422; NID:g146255; PIDN:AAA23929.1; PID:g146257
C:Comment: The gene coding for this protein is located between the gpt and phoE genes.
C:Genetics:
A:Gene: yafA
A:Map position: 6 min
C:Superfamily: yafA protein

Query Match      100.0%; Score 23; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EILDV 5
      .|||||
Db     65 EILDV 69

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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:20:02 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-251-073a-16

Perfect score: 23

Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 82

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	107	1 YAAK_BACSU	P24281 bacillus su
2	23	100.0	121	1 PAND_WOLSU	O34246 wolinnella s
3	23	100.0	156	1 GREU_UREPA	Q9PQ17 ureaplasma
4	23	100.0	172	1 STEL_DROME	P15021 drosophila
5	23	100.0	177	1 YA50_METJA	Q58450 methanococc
6	23	100.0	198	1 IPE2_ARATH	O4663 arabidopsis
7	23	100.0	217	1 NODB_RHIME	P02963 rhizobium m
8	23	100.0	229	1 ACHP_LYMST	P58154 lymanaea sta
9	23	100.0	259	1 DUBA_MOUSE	Q9GY15 mus musculu
10	23	100.0	262	1 NASD_KLEPN	P39459 klebsiella
11	23	100.0	267	1 YFAU_ECOLI	P76459 escherichia
12	23	100.0	271	1 PURR_LACLA	O53065 lactococcus
13	23	100.0	285	1 ATPG_BACP3	P02922 bacillus ps
14	23	100.0	287	1 ATPG_BACCA	P41010 bacillus ca
15	23	100.0	287	1 ATPG_BACST	Q92007 bacillus st
16	23	100.0	289	1 UBIG_RICCN	Q92007 rickettsia
17	23	100.0	307	1 CRTB_SYNP7	P37269 synchococc
18	23	100.0	320	1 Y054_MYCPN	P75049 mycoplasma
19	23	100.0	332	1 SD22_SCHPO	P22194 schistosach
20	23	100.0	338	1 DHAS_SHESP	Q56732 shewanella
21	23	100.0	338	1 DHAS_SHEVI	Q56734 shewanella
22	23	100.0	342	1 LYC_CLOPE	P26836 clostridium
23	23	100.0	344	1 FLIG_BORBU	P52610 borrelia bu
24	23	100.0	351	1 DJB2_HUMAN	P25686 homo sapien
25	23	100.0	365	1 DP3B_ECOLI	P00583 escherichia
26	23	100.0	366	1 DP3B_SALTY	P26464 salmonella
27	23	100.0	380	1 P37_MYCPN	P75371 mycoplasma
28	23	100.0	380	1 RPA2_ARCFU	Q28390 archaeoglob
29	23	100.0	380	1 YKEP_BACSU	P54955 bacillus su
30	23	100.0	387	1 2A5E_MOUSE	Q61151 m serine/th
31	23	100.0	394	1 CEGT_HUMAN	Q66739 homo sapien
32	23	100.0	414	1 YAFB_ECOLI	P04335 escherichia
33	23	100.0	414	1 YAFB_SALTY	P37722 salmonella

34	23	100.0	435	1 2A5G_MOUSE	O60996 m serine/th
35	23	100.0	467	1 2A5E_HUMAN	Q16337 h serine/th
36	23	100.0	472	1 YAPI_MOUSE	P46938 mus musculu
37	23	100.0	484	1 DCOR_NEUCR	P27121 neurospora
38	23	100.0	486	1 2ASA_HUMAN	Q15172 h serine/th
39	23	100.0	493	1 PVBS_DROME	Q01637 drosophila
40	23	100.0	497	1 2ASB_HUMAN	Q15173 homo sapien
41	23	100.0	500	1 2ASB_RABIT	Q28647 o serine/th
42	23	100.0	503	1 GLPK_PSETO	O87924 pseudomonas
43	23	100.0	506	1 SYG_DEIRA	Q98955 deinococcus
44	23	100.0	522	1 PINC_CANPA	Q28375 canis fami
45	23	100.0	522	1 PINC_HORSE	Q28377 equus cabal
46	23	100.0	524	1 2A5G_HUMAN	Q13362 h serine/th
47	23	100.0	524	1 2A5G_RABIT	Q28651 o serine/th
48	23	100.0	551	1 SYM_CHLPN	Q92959 chlamydia p
49	23	100.0	586	1 2A5D_RABIT	Q28653 o serine/th
50	23	100.0	602	1 2A5D_HUMAN	Q14738 h serine/th
51	23	100.0	690	1 TOP1_BACHD	Q9k23 bacillus ha
52	23	100.0	709	1 ETP2_FOWPV	Q9J562 fowlpox vir
53	23	100.0	719	1 DEND_RAT	P50617 rattus norv
54	23	100.0	784	1 TLR2_BOVIN	O951a9 bos taurus
55	23	100.0	784	1 TLR2_HUMAN	O60603 homo sapien
56	23	100.0	796	1 TLR6_HUMAN	O9y2c9 homo sapien
57	23	100.0	819	1 ADVL_HUMAN	O75366 homo sapien
58	23	100.0	861	1 LON_TREPA	O83336 treponema p
59	23	100.0	889	1 IREI_HUMAN	P21399 homo sapien
60	23	100.0	902	1 RNE_BUCAI	P57429 buchnera ap
61	23	100.0	919	1 SYNFP_HUMAN	O9y6h5 homo sapien
62	23	100.0	923	1 HEPB_HAEIN	P44781 haemophilus
63	23	100.0	949	1 GLND_RHIME	P56884 rhizobium m
64	23	100.0	952	1 YK15_CABEL	P46012 caenorhabdi
65	23	100.0	1021	1 SECA_ARATH	Q98y10 arabidopsis
66	23	100.0	1027	1 KINN_MOUSE	P33175 mus musculu
67	23	100.0	1032	1 KINN_HUMAN	Q12840 homo sapien
68	23	100.0	1032	1 YGPK_ECO57	Q8x475 escherichia
69	23	100.0	1032	1 YGPK_ECOLI	Q46811 escherichia
70	23	100.0	1036	1 SECA_SFLOL	Q36795 spinacia ol
71	23	100.0	1191	1 DNBI_MCMVS	P30672 murine cyto
72	23	100.0	1197	1 EVGS_ECO57	P58402 escherichia
73	23	100.0	1197	1 EVGS_ECOLI	P30855 escherichia
74	23	100.0	1317	1 RPOD_SYNY3	P73334 synchococyt
75	23	100.0	1370	1 DP2L_HALN1	Q9hm88 halobacteri
76	23	100.0	1862	1 ANKI_MOUSE	Q02357 mus musculu
77	23	100.0	1880	1 ANKI_HUMAN	P16157 homo sapien
78	23	100.0	2265	1 PINC_BOVIN	P07589 bos taurus
79	23	100.0	2386	1 PINC_HUMAN	P02751 homo sapien
80	23	100.0	2477	1 PINC_MOUSE	P11276 mus musculu
81	23	100.0	2477	1 PINC_RAT	P04937 rattus norv
82	23	100.0	2481	1 PINC_XENLA	Q91740 xenopus lae

ALIGNMENTS

RESULT 1
YAAK_BACSU STANDARD; PRT; 107 AA.
ID YAAK_BACSU STANDARD; PRT; 107 AA.
AC P24281;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yaak.
GN YAAK.
OS Bacillus subtilis.
OC Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP MEDLINE=91088245; PubMed=2124672;
RX Alonso C., Shirahige K., Ogasawara N.;
RA "Molecular cloning, genetic characterization and DNA sequence
RT analysis of the recM region of Bacillus subtilis.";
RL Nucleic Acids Res. 18:6771-6777(1990).


```

RX MEDLINE=20500219; PubMed=11048724;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum.";
RL Nature 407:757-762(2000).
CC -1- FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION
CC ELONGATION FAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING
CC SITES IN DNA HAVE THE PROPERTY OF TRAPPING A CERTAIN FRACTION
CC OF ELONGATING RNA POLYMERASES THAT PASS THROUGH, RESULTING IN
CC LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIPT BY
CC CLEAVAGE FACTORS SUCH AS GRE A OR GRE B ALLOWS THE RESUMPTION OF
CC ELONGATION FROM THE NEW 3' TERMINUS. GRE A RELEASES SEQUENCES OF
CC 2 TO 3 NUCLEOTIDES (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GRE A/GRE B FAMILY.
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CC
CC EMBL; AB002128; AAF30713.1; -
CC HSSP; P21346; 1GRJ.
CC InterPro; IPR001437; GreA_Greb.
CC Pfam; PF01272; GreA_Greb; 1.
CC Pfam; PF03449; GreA_Greb_N; 1.
CC ProDom; PD004918; GreA_Greb; 1.
CC PROSITE; PS00829; GREAB_1; 1.
CC PROSITE; PS00830; GREAB_2; FALSE NEG.
CC Transcription regulation; DNA-binding; Coiled coil; Complete proteome.
CC DOMAIN 7 24 COILED COIL (POTENTIAL).
CC DOMAIN 42 84 COILED COIL (POTENTIAL).
CC SEQUENCE 156 AA; 17767 MW; 86BEA8EC07C96461 CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 156;
CC Best Local Similarity 100.0%; Pred. No. 77;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 1 BILDV 5
CC Db 20 BILDV 24
CC
CC RESULT 4
CC STEL_DROME STANDARD; PRT; 172 AA.
CC
CC AC P15021;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC DE Stellate protein.
CC GN STB.
CC OS Drosophila melanogaster (Fruit fly).
CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
CC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
CC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_TaxID=7227;
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN=Oregon-R; TISSUE=Testis;
CC RX MEDLINE=90169476; PubMed=1689686;
CC RA Livak K.J.;
CC RT "Detailed structure of the Drosophila melanogaster stellate genes and
CC their transcripts.";
CC RL Genetics 124:303-316(1990).
CC -1- FUNCTION: RESPONSIBLE FOR THE APPEARANCE OF PROTEINACEOUS STAR-
CC SHAPED CRYSTALS IN THE PRIMARY SPERMATOCYTES OF D.MELANOGASTER
CC MALES LACKING A Y CHROMOSOME.
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE COPIES OF THE STELLATE GENE IN
CC FRUIT FLY.

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CC -1- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
CC
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CC
CC EMBL; X15899; CAA33906.1; -
CC PIR; S08120; S08120.
CC PIR; S24397; S24397.
CC FlyBase; FBgn0003523; Ste.
CC InterPro; IPR000704; CAS_kinase_II.
CC Pfam; PF01214; CK II beta; 1.
CC PRINTS; PR00472; CASKINASEII.
CC PROSITE; PS01101; CK2_BETA; 1.
CC testis; Multigene family.
CC SQ SEQUENCE 172 AA; 19507 MW; C86304F591E76F8A CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 172;
CC Best Local Similarity 100.0%; Pred. No. 85;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Qy 1 BILDV 5
CC Db 46 BILDV 50
CC
CC RESULT 5
CC YASO_METJA STANDARD; PRT; 177 AA.
CC ID YASO_METJA
CC AC Q58450;
CC DT 15-JUL-1998 (Rel. 36, Created)
CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Hypothetical protein MJ1050.
CC GN MJ1050.
CC OS Methanococcus jannaschii.
CC Archaea; Euryarchaeota; Methanococci; Methanococcales;
CC OC Methanocaldococcaceae; Methanocaldococcus.
CC NCBI_TaxID=2190;
CC RN [1]
CC SEQUENCE FROM N.A.
CC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
CC RX MEDLINE=96337999; PubMed=8688087;
CC RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
CC Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
CC Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
CC Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
CC Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
CC Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
CC Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
CC Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
CC RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
CC jannaschii.";
CC RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: BELONGS TO THE UPF0101 FAMILY.
CC
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CC
CC EMBL; U67548; AAB99053.1; -
CC TIGR; MJ1050;
CC InterPro; IPR001977; Depp_CoKinase.
CC Pfam; PF01121; Coas; 1.
CC Hypothetical protein; ATP-binding; Complete proteome.

```

FT NP_BIND 7 14 ATP (POTENTIAL).
 SQ SEQUENCE 177 AA; 20690 MW; F209572AA79CD2F9 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 177;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db 118 EILDV 122
 RESULT 6
 IFE2 ARATH
 ID IFE2 ARATH STANDARD; PRT; 198 AA.
 AC 004663; Q9SANS;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Eukaryotic translation initiation factor 4E (eIF4E) (mRNA
 DE cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(ISO)4F P28
 DE subunit) (eIF4E180 protein).
 GN EIF4E2 OR ATG535620 OR MJEA4.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97378268; PubMed=9234949;
 RA Wittmann S., Chatel H., Fortin M.G., Laliberte J.F.;
 RT "Interaction of the viral protein genome linked of turnip mosaic
 RT potyvirus with the translational eukaryotic initiation factor (iso)
 RT 4E of Arabidopsis thaliana using the yeast two-hybrid system.";
 RL Virology 234:84-92(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rodriguez C., Freire M.A., Robaglia C.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98403884; PubMed=9734815;
 RA Kocani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 CC -1- FUNCTION: RECOGNIZES AND BINDS THE 7-METHYLGUANOSINE-CONTAINING
 CC MRNA "CAP" DURING AN EARLY STEP IN THE INITIATION OF PROTEIN
 CC SYNTHESIS AND FACILITATES RIBOSOME BINDING BY INDUCING THE
 CC UNWINDING OF THE MRNA SECONDARY STRUCTURES (BY SIMILARITY).
 CC -1- SUBUNIT: EIF4F IS A TRIMER COMPOSED OF EIF4E, EIF4G AND EIF4A
 CC (WHICH CAN CYCLE IN AND OUT OF THE COMPLEX). IN HIGHER PLANTS TWO
 CC ISOFORMS OF EIF4F HAVE BEEN IDENTIFIED, NAMED EIF4F AND
 CC EIF (ISO)4F. EIF4F HAS SUBUNITS P220 AND P28, WHEREAS EIF-(ISO)4F
 CC HAS SUBUNITS P82 AND P26 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE EUKARYOTIC INITIATION FACTOR 4E FAMILY.
 CC -----
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 CC -----
 CC EMBL; U62044; AAB66906.1; ALT_INIT.
 CC EMBL; Y10547; CRA71579.1; --
 CC EMBL; AB013393; BAB09303.1; --
 CC HSSP; P07260; 1AP8.

DR InterPro: IPR001040; TIF_eIF_4E.
 DR Pfam: PF01652; IF4E; 1.
 DR ProDom: PD003697; TIF_eIF_4E; 1.
 DR PROSITE: PS00813; IF4E; 1.
 KW Initiation factor; Protein biosynthesis; RNA-binding;
 KW Multigene family.
 SQ SEQUENCE 198 AA; 22514 MW; 71FEB309E073A9D2 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 198;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db 175 EILDV 179
 RESULT 7
 NODB RHIME
 ID NODB RHIME STANDARD; PRT; 217 AA.
 AC P02963; O52477;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Chitooligosaccharide deacetylase (EC 3.5.1.-) (Modulation protein B).
 GN NODB OR RA0474 OR SMA0868.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OG Plasmid pSymA (megaplasmid 1).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=85229955; PubMed=4006668;
 RA Egelhoff T.T., Fisher R.F., Jacobs T.W., Mulligan J.T., Long S.R.;
 RT "Nucleotide sequence of Rhizobium meliloti 1021 modulation genes:
 RT nodD is read divergently from nodABC.";
 RL DNA 4:241-248(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=41;
 RX MEDLINE=85087953; PubMed=6336331;
 RA Teocek I., Kondorosi E., Stepkowski T., Posfai J., Kondorosi A.;
 RT "Nucleotide sequence of Rhizobium meliloti modulation genes.";
 RL Nucleic Acids Res. 12:9509-9524(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=042B;
 RA Yang X., Gao W.M., Yang S.S.;
 RT "The complete sequence of S. meliloti 042B nodABC.";
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 RT Sinorhizobium meliloti pSymA megaplasmid";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 CC -1- FUNCTION: IS INVOLVED IN GENERATING A SMALL HEAT-STABLE COMPOUND
 CC (NOD), AN ACYLATED OLIGOMER OF N-ACETYLGLUCOSAMINE, THAT
 CC STIMULATES MITOSIS IN VARIOUS PLANT PROTOPLASTS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: TO OTHER POLYSACCHARIDE DEACETYLASES.
 CC -----
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DR EMBL; M11268; A989361.1; -;
 DR EMBL; X01649; CAA25809.1; -;
 DR EMBL; AF038577; AAB95330.1; -;
 DR EMBL; AB007237; AAK65132.1; -;
 DR PIR; A03483; ZZZRBM.
 DR PIR; A03484; ZZZRBM4.
 DR InterPro; IPR002509; Polysac_deacet.
 DR Pfam; PF01522; Polysac_deacet; 1.
 KW Hydrolase; Nodulation; Plasmid; Complete proteome.
 FT VARIANT 10 10 V -> M (IN STRAIN 41).
 FT VARIANT 59 59 A -> T (IN STRAIN 41).
 FT VARIANT 116 116 H -> R (IN STRAIN 41).
 FT VARIANT 195 198 ALSR -> GPV (IN STRAIN 042B).
 FT CONFLICT 108 118 ACPOAAVRHRI -> LVLRPSDYIE (IN REF. 1).
 SQ SEQUENCE 217 AA; 23671 MW; 01F82A0C75EA662D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 38 EILDV 42

RESULT 8

ACHP LYNST
 ID ACHP LYNST STANDARD; PRT; 229 AA.
 AC P58154;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholine-binding protein precursor (ACh-binding protein) (ACHBP).
 OS *Lymnaea stagnalis* (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
 OC Lymnaeidae; Lymnaea.
 OX NCBI_TaxID=6523;
 RN [1]
 RP SEQUENCE FROM N.A., SEQUENCE OF 20-30, AND MASS SPECTROMETRY.
 RC TISSUE=CNS;
 RX MEDLINE=21256198; PubMed=11357121;
 RA Smit A.B., Syed N.I., Schaap D., van Minnen J., Klumperman J.,
 RA Kits K.S., Lodder H., van Der Schors R.C., van Elk R., Sorgedraeger B.,
 RA Brejc K., Sixma T.K., Geraerts W.P.M.;
 RT "A glia-derived acetylcholine-binding protein that modulates synaptic
 RT transmission.";
 RL Nature 411:261-268(2001).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 20-229.
 RX MEDLINE=21256199; PubMed=11357122;
 RA Brejc K., van Dijk W.J., Klaassen R.V., Schuurmans M.,
 RA van Der Oost J., Smit A.B., Sixma T.K.;
 RT "Crystal structure of an ACh-binding protein reveals the
 RT ligand-binding domain of nicotinic receptors.";
 RL Nature 411:269-276(2001).

CC -1- FUNCTION: BINDS TO ACETYLCHOLINE. MODULATES NEURONAL SYNAPTIC
 CC TRANSMISSION.
 CC -1- SUBUNIT: HOMOPENTAMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED. RELEASED IN AN ACETYLCHOLINE-
 CC DEPENDENT MANNER IN THE SYNAPTIC CLEFT.
 CC -1- TISSUE SPECIFICITY: EXPRESSED BY GLIAL CELLS.
 CC -1- PFM: N-GLYCOSYLATED.
 CC -1- MASS SPECTROMETRY: MW=24720.4; METHOD=QTOF; RANGE=20-229.
 CC -1- SIMILARITY: TO THE EXTRACELLULAR PORTION OF LIGAND-GATED IONIC
 CC CHANNELS FAMILY.

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DR EMBL; AF364899; AAK64377.1; -;
 DR PDB; 119B; 16-MAY-01.
 DR InterPro; IPR001175; Neur channel.
 DR Pfam; PF02931; Neur chan IBD; 1.
 KW Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 1 229 ACETYLCHOLINE-BINDING PROTEIN.
 FT DISULFID 142 155
 FT DISULFID 207 207
 FT CARBOHYD 85 85 N-LINKED (GLCNAC...) (PROBABLE).
 SQ SEQUENCE 229 AA; 26061 MW; B76A3A13E7EF8FCB CRC64;

Query Match 100.0%; Score 23; DB 1; Length 229;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 191 EILDV 195

RESULT 9

DJBA MOUSE
 ID DJBA_MOUSE STANDARD; PRT; 259 AA.
 AC Q9QYI5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DnaJ homolog subfamily B member 10 (mD38).
 GN DnaJb10.
 OS *Mus musculus* (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=21023480; PubMed=11147971;
 RA Ohtsuka K., Hata M.;
 RT "Mammalian HSP40/DNAJ homologs: cloning of novel cDNAs and a proposal
 RT for their classification and nomenclature.";
 RL Cell Stress Chaperones 5:98-112(2000).
 CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.

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DR EMBL; AB028858; BAA88306.1; -;
 DR HSP; P25685; IHUJ.
 DR MGD; MGI:1928739; DnaJb10.
 DR InterPro; IPR001623; DnaJ N.
 DR InterPro; IPR002950; Josephin.
 DR InterPro; IPR003903; UIM.
 DR Pfam; PF00226; DnaJ; 1.
 DR Pfam; PF02809; UIM; 2.
 DR SMART; SM00271; DnaJ; 1.
 DR PROSITE; PS00636; DnaJ 1; FALSE_NEG.
 DR PROSITE; PS50076; DnaJ_2; 1.

KW Chaperone.
 FT DOMAIN 3 71 J-DOMAIN.
 FT DOMAIN 133 140 POLY-SER.
 SQ SEQUENCE 259 AA; 28601 MW; 81387B09ADF9B09A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|||||
Db 6 EILDV 10

RESULT 10

NASD_KLEPN STANDARD; PRT; 262 AA.
AC P39459;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitrate transport protein nasd.
GN NASD.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M5a1;
RX MEDLINE=94222832; PubMed=8169203;
RA Lin J.T., Goldman B.S., Stewart V.;
RT "The nasPDCBA operon for nitrate and nitrite assimilation in
Klebsiella pneumoniae M5a1".
RL J. Bacteriol. 176:2551-2559(1994).
[2]
RP REVISIONS.
RC STRAIN=M5a1;
RA Stewart V.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PROBABLY PART OF A HIGH-AFFINITY BINDING-PROTEIN-
DEPENDENT TRANSPORT SYSTEM FOR NITRATE. PROBABLY RESPONSIBLE FOR
ENERGY COUPLING TO THE TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
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CC -----
DR EMBL; L27431; AAB86901.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01184; ntrCD; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
DR Transport; ATP-binding; Membrane; Nitrate assimilation.
FT NP_BIND 41 48 ATP (POTENTIAL).
SQ SEQUENCE 262 AA; 28996 MW; AD1B32490A2AEA10 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|||||
Db 222 EILDV 226

RESULT 11

YFAU_ECOLI STANDARD; PRT; 271 AA.

ID YFAU_ECOLI STANDARD; PRT; 267 AA.
AC P76459; P76925; P76926; P76928; P76929;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yfaU.
GN YFAU OR B2245.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12".
RL Science 277:1453-1474 (1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
K-12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features".
RL DNA Res. 4:91-113(1997).
CC -1- SIMILARITY: BELONGS TO THE HPCH/HPAI ALDOLASE FAMILY.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 117.

CC -----
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CC -----
DR EMBL; A8000314; AAC75305.1; -.
DR EMBL; D30855; BAA16064.1; -.
DR EMBL; D30855; BAA16065.1; ALT_FRAME.
DR EMBL; D30856; BAA16068.1; ALT_FRAME.
DR EMBL; D30856; BAA16069.1; ALT_FRAME.
DR HSPSP; P23522; 1DXE.
DR EcoGene; EG14083; yfaU.
DR InterPro; IPR005000; Hpch_Hpai.
DR Pfam; PF03328; Hpch_Hpai; 1.
DR Hypothetical protein; Lyase; Complete proteome.
SQ SEQUENCE 267 AA; 28916 MW; F68506D8A11D23FE CRC64;

Query Match 100.0%; Score 23; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|||||
Db 163 EILDV 167

RESULT 12

PURR_LACLA STANDARD; PRT; 271 AA.
ID PURR_LACLA
AC O53065;
DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 GN Pur operon repressor.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis), and
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360, 1359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.1.lactis; STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=1137471;
 RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403";
 RL Genome Res. 11:731-753(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=L.1.cremoris; STRAIN=MG1363;
 RA Kilstrup M.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CONTROLS TRANSCRIPTION OF THE PUR OPERON FOR PURINE
 CC BIOSYNTHETIC GENES (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE
 CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ222642; CAA10902.1; -;
 DR EMBL; AE006455; AAK06357.1; -;
 DR InterPro; IPR000836; PRtransferase.
 DR InterPro; IPR002375; Pr/py rp trans.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR PROSITE; PS00103; PUR PYR PR TRANSFER; FALSE NEG.
 KW DNA-binding; Transcription regulation; Repressor; Complete proteome.
 SQ SEQUENCE 271 AA; 30361 MW; 04614AA24E1C4BCD CRC64;

 Query Match 100.0%; Score 23; DB 1; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 148 EILDV 152

 RESULT 13
 ID ATFG BACFP3 STANDARD; PRT; 286 AA.
 AC P09222;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ATP synthase gamma chain precursor (EC 3.6.3.14).
 GN ATPG.
 OS Bacillus PS3 (Thermophilic bacterium PS-3).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=70306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=88163679; PubMed=2894854;
 RX Ohta S., Yoshida M., Ishizuka M., Hirata H., Hamamoto T.,
 RA Otawara-Hamamoto Y., Matsuda K., Kagawa Y.;
 RT "Sequence and over-expression of subunits of adenosine triphosphate
 RT synthase in thermophilic bacterium PS3";
 RL Biochim. Biophys. Acta 933:141-155(1988).

CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
 CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
 CC THROUGH THE CF(0) COMPLEX.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out)
 CC -1- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
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 CC -----
 DR EMBL; X07804; CAA30653.1; -;
 DR PIR; S01402; S01402.
 DR InterPro; IPR000131; ATPase_gamma.
 DR Pfam; PF00231; ATP-synt; 1.
 DR PRINTS; PRO0126; ATPASEGAMMA.
 DR TIGRFAMS; TIGR01146; ATPsyn_Figamma; 1.
 DR PROSITE; PS00153; ATPASE GAMMA; 1.
 KW Hydrolase; ATP synthesis; CF(1); Hydrogen ion transport.
 FT PROPEP 1 4
 FT CHAIN 1 5 286 ATP SYNTHASE GAMMA CHAIN.
 SQ SEQUENCE 286 AA; 32248 MW; ABB96F687C999252 CRC84;

 Query Match 100.0%; Score 23; DB 1; Length 286;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 212 EILDV 216

 RESULT 14
 ID ATFG BACCA STANDARD; PRT; 287 AA.
 AC P41010;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ATP synthase gamma chain (EC 3.6.3.14).
 GN ATPG.
 OS Bacillus caldotenax.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1395;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ishizuka M.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE
 CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS
 CC THROUGH THE CF(0) COMPLEX.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -1- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.
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EMBL; D38058; BAA07247.1; -;
DR InterPro; IPR000131; ATPase_gamma.
DR Pfam; PF00231; ATP-synt; 1.
DR PRINTS; PR00126; ATPASEGAMMA.
DR TIGRFAMs; TIGR01146; ATPsyn_Figamma; 1.
DR PROSITE; PS00153; ATPASE_GAMMA; FALSE_NEG.
KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase.
SQ SEQUENCE 287 AA; 32343 MW; BA039503BD1F1E5A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|||||
DB 213 EILDV 217

RESULT 15
ID ATPG_BACST STANDARD; PRT; 287 AA.
AC P42007;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase gamma chain (EC 3.6.3.14).
GN ATPG.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP Sequence from N.A.
RA Ishizuka M., Imai H.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.
CC 1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate + H(+) (out).
CC 1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
CC 1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.

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EMBL; D38060; BAA07254.1; -;
DR InterPro; IPR000131; ATPase_gamma.
DR Pfam; PF00231; ATP-synt; 1.
DR PRINTS; PR00126; ATPASEGAMMA.
DR TIGRFAMs; TIGR01146; ATPsyn_Figamma; 1.
DR PROSITE; PS00153; ATPASE_GAMMA; FALSE_NEG.
KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase.
SQ SEQUENCE 287 AA; 32391 MW; 78A9FB92E01BAE6E CRC64;

Query Match 100.0%; Score 23; DB 1; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|||||

DB 213 EILDV 217
RESULT 16
ID UBIG_RICCN STANDARD; PRT; 289 AA.
AC Q92H07;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 3-demethylubiquinone-9 3-methyltransferase (EC 2.1.1.64) (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHHB methyltransferase).
GN UBIG OR RC0965.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
RL 1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 3-demethylubiquinone-9 = S-adenosyl-L-homocysteine + ubiquinone-9.
CC 1- PATHWAY: Ubiquinone biosynthesis.
CC 1- SIMILARITY: BELONGS TO THE UBIG/COQ3 FAMILY.
CC 1- SIMILARITY: CONTAINS 1 RPE1 INSERT DOMAIN.

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EMBL; AE008649; AAL03503.1; -;
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR000051; SAM_bind.
DR TIGRFAMs; TIGR01045; RPE; 1.
KW Ubiquinone biosynthesis; Transferase; Methyltransferase; Complete proteome.
FT DOMAIN 50 98 RPE1 INSERT.
SQ SEQUENCE 289 AA; 33074 MW; 4CAEA6827EC7B977 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|||||
DB 104 EILDV 108

RESULT 17
ID_CRTB_SYNP7 STANDARD; PRT; 307 AA.
AC P37269;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phytoene synthase (EC 2.5.1.-).
GN CRTB OR PYS.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=1140;
RN [1]
RP SEQUENCE FROM N.A.


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RX MEDLINE=92164786; PubMed=1537409;
RA Chamovitz D., Misawa D., Sandmann N., Hirschberg J.;
RT "Molecular cloning and expression in Escherichia coli of a
RT cyanobacterial gene coding for phytoene synthase, a carotenoid
RT biosynthesis enzyme.";
RL FEBS Lett. 296:305-310(1992).
CC -1- FUNCTION: CATALYZES THE REACTION FROM PREPHYTOENE DIPHOSPHATE
CC TO PHYTOENE.
CC -1- CATALYTIC ACTIVITY: 2 geranylgeranyl diphosphate = diphosphate +
CC prephytoene diphosphate.
CC -1- CATALYTIC ACTIVITY: Prephytoene diphosphate = diphosphate +
CC phytoene.
CC -1- PATHWAY: Carotenoid biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE PHYTOENE/SQUALENE SYNTHETASE FAMILY.
CC
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CC
DR EMBL; X63873; CAA45350.1; -.
DR PIR; S22200; S22200.
DR PIR; S20383; S20383.
DR InterPro; IPR02060; Squ/phyt_synthese.
DR Pfam; PF00494; SQS_PSY; 1.
DR PROSITE; PS01044; SQUALENE_PHYTOEN_SYN_1; 1.
DR PROSITE; PS01045; SQUALENE_PHYTOEN_SYN_2; 1.
KW Multifunctional enzyme; Carotenoid biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 35781 MW; A13B425F66D10EB8 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 269 EILDV 273

RESULT 18
Y054 MYCPN STANDARD; PRT; 320 AA.
AC P75049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein MG054 homolog (D09_orf320).
GN MPN067 OR MP087.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelsreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY, AND PARTIAL SEQUENCE.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=21089919; PubMed=11271496;
RA Regula J.T., Ueberle B., Boguth G., Goerg A., Schnoelzer M.,
RA Herrmann R., Frank R.;
RT "Towards a two-dimensional proteome map of Mycoplasma pneumoniae.";
RL Electrophoresis 21:3765-3780(2000).
CC -1- SIMILARITY: BELONGS TO THE NUSG FAMILY.
CC

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CC
DR EMBL; AE000011; AAB95735.1; -.
DR InterPro; IPR001062; NusG.
DR Pfam; PF02357; NusG; 1.
KW Complete proteome.
SQ SEQUENCE 320 AA; 36107 MW; EC3C626C8EAB63F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 320;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 38 EILDV 42

RESULT 19
SD22 SCHPO STANDARD; PRT; 332 AA.
AC P22134;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatases PPI regulatory subunit sds22.
GN SDS22 OR SPAC4A8.12C.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91098642; PubMed=1846086;
RA Ohkura H., Yanagida M.;
RT "S. pombe gene sds22+ essential for a midmitotic transition encodes a
RT leucine-rich repeat protein that positively modulates protein
RT phosphatase-1.";
RL Cell 64:149-157(1991).
RN [2]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RA Stone E.M., Yamano H., Kinoshita N., Yanagida M.;
RT "Mitotic regulation of protein phosphatases by the fission yeast
RT sds22 protein.";
RL Curr. Biol. 3:13-26(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd J., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

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RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880 (2002).
CC -1- FUNCTION: ESSENTIAL FOR THE MITOTIC METAPHASE/ANAPHASE TRANSITION.
CC POSITIVELY MODULATES PROTEIN PHOSPHATASE-1. POSSIBLY BY FORMING A
CC REPEATING HELICAL ROD THAT IS CAPABLE OF ENHANCING A PPI-DEPENDENT
CC DEPHOSPHORYLATION ACTIVITY.
CC -1- SUBUNIT: PHYSICALLY INTERACTS WITH THE DIS2 AND SDS21
CC PHOSPHATASES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- PTM: PHOSPHORYLATED.
CC -1- SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: STRONG, TO YEAST SDS22 AND C.ELEGANS T09A5.9.
CC -----
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CC -----
CC EMBL; M57495; AAA35342.1; ALT_INIT.
CC EMBL; Z98762; CAB11482.1; -.
CC PIR; A38439; A38439.
CC HSSP; P09661; 1A9N.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR003592; LRR.out.
CC InterPro; IPR003603; LRRcap.
CC Pfam; PF00560; LRR; 8.
CC SMART; SM00370; LRR; 10.
CC SMART; SM00446; LRRcap; 1.
CC Leucine-rich repeat; Repeat; Mitosis; Nuclear protein;
KW Phosphorylation.
FT REPEAT 20 44 LRR 1.
FT REPEAT 61 86 LRR 2.
FT REPEAT 103 127 LRR 3.
FT REPEAT 147 171 LRR 4.
FT REPEAT 191 215 LRR 5.
FT REPEAT 217 236 LRR 6.
FT REPEAT 237 260 LRR 7.
FT REPEAT 284 307 LRR 8.
SQ SEQUENCE 332 AA; 38066 MW; CF7FBAD984E2A345 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 240 EILDV 244
|||||
RESULT 20
DHAS SHESP
ID DHAS SHESP STANDARD; PRT; 338 AA.
AC Q56732;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase)
DE (ASADH).
GN ASD.
OS Shewanella sp. (strain DB6705).
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Shewanella.
OX NCBI_TaxID=126830;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=97306055; PubMed=9163523;
RA Kato C., Smorawinska M., Li L., Horikoshi K.;
RT "Comparison of the gene expression of aspartate beta-D-semialdehyde
RT dehydrogenase at elevated hydrostatic pressure in deep-sea bacteria.";
RL J. Biochem. 121:717-723 (1997).
CC -1- CATALYTIC ACTIVITY: L-aspartate-4-semialdehyde + phosphate +
CC NADP(+) = L-4-aspartyl phosphate + NADPH.
CC -1- PATHWAY: SECOND STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
CC FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
CC TO MET, TO ILE AND TO THR.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE
CC FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D49539; BAA08488.1; -.
CC HSSP; P00353; 1BRM.
CC InterPro; IPR000319; Asp_semiald_dh.
CC InterPro; IPR000534; Semialdh_dh.
CC Pfam; PF01118; Semialdehyde_dh; 1.
CC Pfam; PF02774; Semialdehyde_dhc; 1.
CC TIGRFAMs; TIGR01296; asd_B; 1.
CC PROSITE; PS01103; ASD; FALSE NEG.
KW Oxidoreductase; NADP; Diaminopimelate biosynthesis;
KW Lysine biosynthesis.
KW ACT_SITE 132 132 BY SIMILARITY.
SQ SEQUENCE 338 AA; 36984 MW; 6BCD8921E4977185 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 55 EILDV 59
|||||
RESULT 21
DHAS SHEVI
ID DHAS SHEVI STANDARD; PRT; 338 AA.
AC Q56734;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase)
DE (ASADH).
GN ASD.
OS Shewanella violacea.
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Shewanella.
OX NCBI_TaxID=60217;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSS12;
RX MEDLINE=97306055; PubMed=9163523;
RA Kato C., Smorawinska M., Li L., Horikoshi K.;
RT "Comparison of the gene expression of aspartate beta-D-semialdehyde
RT dehydrogenase at elevated hydrostatic pressure in deep-sea bacteria.";
RL J. Biochem. 121:717-723 (1997).
CC -1- CATALYTIC ACTIVITY: L-aspartate-4-semialdehyde + phosphate +
CC NADP(+) = L-4-aspartyl phosphate + NADPH.
CC -1- PATHWAY: SECOND STEP IN THE COMMON BIOSYNTHETIC PATHWAY LEADING
CC FROM ASP TO THE CELL WALL PRECURSOR MESO-DIAMINOPIMELATE, TO LYS,
CC TO MET, TO ILE AND TO THR.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -----

CC -1- SIMILARITY: BELONGS TO THE ASPARTATE-SEMIALDEHYDE DEHYDROGENASE
FAMILY.

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CC or send an email to license@sib-sib.ch).

CC -----

DR EMBL; D49540; BAA08490.1; -;
DR HSPSP; P00353; 1BRM.

DR InterPro; IPR000319; Asp_semiald dh.
DR InterPro; IPR000534; Semialdh dh.
DR Pfam; PF01118; Semialdehyde dh; 1.
DR Pfam; PF02774; Semialdehyde dhc; 1.
DR TIGRFAMs; TIGR01296; and B; 1.
DR PROSITE; PS01103; ASD; Diaminopimelate biosynthesis;
KW Oxidoreductase; NADP; Diaminopimelate biosynthesis;
FT Lysine biosynthesis.
KW ACT SITE 132 132 BY SIMILARITY.
SQ SEQUENCE 338 AA; 37061 MW; 80DDC1P46AEAF30AC CRC64;

Query Match 100.0%; Score 23; DB 1; Length 338;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BILDV 5
|
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|
|
Db 55 EILDV 59

RESULT 22
LYC_CLOPE
ID LYC_CLOPE STANDARD; PRT; 342 AA.
AC P26836;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable autolytic lysozyme (EC 3.2.1.17) (1,4-beta-N-
DE acetylmuramidase) (Autolysin).
GN LYC OR CPE0382.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohehima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
RN [2]
RP SEQUENCE OF 256-342 FROM N.A.
RC STRAIN=CPN50;
RX MEDLINE=9423189; PubMed=8177218;
RA Canard B., Garnier T., Saint-Joanis B., Cole S.T.;
RT "Molecular genetic analysis of the nagH gene encoding a hyaluronidase
RT of Clostridium perfringens.";
RL Mol. Genet. 243:215-224(1994).

CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC heteropolymers of the prokaryotes cell walls.
CC -1- SIMILARITY: BELONGS TO FAMILY 25 OF GLYCOSYL HYDROLASES.

CC -----

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CC -----

DR EMBL; AP003186; BAB80088.1; -;
DR EMBL; M81878; AAA23261.1; -;
DR InterPro; IPR002053; GH_25.
DR InterPro; IPR003646; SH3_bac.
DR Pfam; PF01183; Glyco_hydro_25; 1.
DR SMART; SM00287; SH3b; 2.
DR PROSITE; PS00953; GLYCOSYL HYDROL F25; 1.
KW Hydrolase; glycosidase; Bacteriolytic enzyme; Repeat;
KW Complete proteome.
FT ACT SITE 13 13 BY SIMILARITY.
FT ACT SITE 40 40 BY SIMILARITY.
FT DOMAIN 230 342 5 X 23 AA TANDEM REPEATS.
FT REPEAT 230 252 1.
FT REPEAT 253 272 2.
FT REPEAT 273 295 3.
FT REPEAT 296 318 4.
FT REPEAT 319 342 5.
SQ SEQUENCE 342 AA; 39557 MW; EC3B4078A2FB4732 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 BILDV 5
|
|
|
|
Db 199 EILDV 203

RESULT 23
FLIG_BORBU
ID FLIG_BORBU STANDARD; PRT; 344 AA.
AC P52610;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar motor switch protein flig.
GN FLIG OR BB0290.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RA Dunn J.J., Butler-Loffredo L., Kieleczawa J., Medalle J., Luft B.J.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Watthey L., McDonald L., Horat K., Roberts K., Hatch B.,
RA Garland S., Fujii C., Cotton M.D., Artiaeh P., Bowman C.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).

CC -1- FUNCTION: FLIG IS ONE OF THREE PROTEINS (FLIG, FLIN, FLIM) THAT
CC FORM A SWITCH COMPLEX THAT IS PROPOSED TO BE LOCATED AT THE BASE
CC OF THE BASAL BODY. THIS COMPLEX INTERACTS WITH THE CHEY AND CHEZ
CC CHEMOTAXIS PROTEINS, IN ADDITION TO CONTACTING COMPONENTS OF THE
CC MOTOR THAT DETERMINE THE DIRECTION OF FLAGELLAR ROTATION (BY
CC SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INNER MEMBRANE-ASSOCIATED (BY
CC SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE FLIG FAMILY.

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EMBL; U43739; AA85613.1; -;
DR EMBL; AE001137; AAC66658.1; -;
DR HSSP; Q9WY63; 1QC7.
DR TIGR; BB0290; -;
DR InterPro; IPR000090; Flg_Motor_Flag.
DR Pfam; PF01706; Flg-C; 1.
DR PRINTS; PR00954; FLGMOTORFLIG.
DR TIGRFAMs; TIGR00207; flig; 1.
KW Chemotaxis; Flagella; Flagellar rotation; Inner membrane;
KW Complete proteome.
SQ SEQUENCE 344 AA; 39006 MW; D6FDCAADFB3AD8D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 344;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 8 EILDV 12

RESULT 24
DJB2_HUMAN
ID _DJB2_HUMAN STANDARD; PRT; 351 AA.
AC P25686;
DT 01-MAY-1992 (Rel. 22, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ homolog subfamily B member 2 (Heat shock 40 kDa protein 3) (DnaJ
protein homolog 1) (HSJ1-1).
GN DNBAB2 OR HSJ1 OR HSPF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92287055; PubMed=1599432;
RA Cheatham M.E.; Brion J.-P.; Anderton B.H.;
RT "Human homologues of the bacterial heat-shock protein DnaJ are
preferentially expressed in neurons.";
RL Biochem. J. 284:469-476(1992).
RN [2]
RP REVISION TO 214.
RA Cheatham M.E.;
RL Submitted (JUL-1998) to the SWISS-PROT data bank.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; HSJ1A AND HSJ1B (SHOWN HERE);
CC -1- TISSUE SPECIFICITY: BRAIN (NEURONAL LAYERS). WEAKLY, IN SKELETAL
CC MUSCLE AND SPLEEN.
CC -1- SIMILARITY: CONTAINS 1 J DOMAIN.
CC
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EMBL; X63368; CAA44968.1; ALT SEQ.
DR EMBL; X63368; CAA44969.1; ALT_SEQ.
DR PIR; S23508; S23508.

DR HSSP; P25685; 1HDJ.
DR Genew; HGNC:5228; DNBAB2.
DR MIM; 604139; -;
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR002950; Josephin.
DR InterPro; IPR003903; UIM.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF02809; UIM; 2.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNBAB2; 1.
DR PROSITE; PS00076; DNBAB2; 1.
KW Chapterone; Neurone; Alternative splicing.
FT DOMAIN 1 71 J-DOMAIN.
FT VARSPIC 275 277 GGR -> DVF (IN ISOFORM HSJ1A).
FT VARSPIC 278 351 MISSING (IN ISOFORM HSJ1A).
SQ SEQUENCE 351 AA; 38783 MW; 1FA290C6764665F3 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 6 EILDV 10

RESULT 25
DP3B_ECOLI
ID _DP3B_ECOLI STANDARD; PRT; 366 AA.
AC P00583;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase III, beta chain (EC 2.7.7.7).
GN DNBAN OR B3701 OR Z5192 OR EGS4636.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84237568; PubMed=6234204;
RA Ohmori H., Kimura M., Negata T., Sakakibara Y.;
RT "Structural analysis of the dnaA and dnaN genes of Escherichia coli.";
RL Gene 28:159-170(1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
genome: organizational symmetry around the origin of replication.";
RL Genomics 16:551-561(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / BDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Tida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [5]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=8298898; PubMed=2841344;
RA Armengod M.E.E., Garcca-Sogo M., Lambies E.;
RT "Transcriptional organization of the *dnaN* and *recF* genes of
RT *Escherichia coli* K-12.";
RL J. Biol. Chem. 263:12109-12114(1988).
RN [6]
RP SEQUENCE OF 143-170 FROM N.A.
RX MEDLINE=86301872; PubMed=3527871;
RA Armengod M.E.E., Lambies E.;
RT "Overlapping arrangement of the *recF* and *dnaN* operons of *Escherichia*
RT *coli*: positive and negative control sequences.";
RL Gene 43:183-196(1986).
RN [7]
RP SEQUENCE OF 297-366 FROM N.A.
RX MEDLINE=84272685; PubMed=6379647;
RA Blonar M.A., Sandler S.J., Armengod M.E., Ream L.W., Clark A.J.;
RT "Molecular analysis of the *recF* gene of *Escherichia coli*.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4622-4626(1984).
RN [8]
RP SEQUENCE OF 342-366 FROM N.A.
RX MEDLINE=84297235; PubMed=6089112;
RA Adachi T., Mizuuchi K., Menzel R., Gellert M.;
RT "DNA sequence and transcription of the region upstream of the *E. coli*
RT *gyrB* gene.";
RL Nucleic Acids Res. 12:6389-6395(1984).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=92257585; PubMed=1349852;
RA Kong X.-P., Onrust R., O'Donnell M., Kuriyan J.;
RT "Three-dimensional structure of the beta subunit of *E. coli* DNA
RT polymerase III holoenzyme: a sliding DNA clamp.";
RL Cell 69:425-437(1992).
RN [10]
RP REVIEW.
RX MEDLINE=92246902; PubMed=1575709;
RA O'Donnell M.;
RT "Accessory protein function in the DNA polymerase III holoenzyme from
RT *E. coli*.";
RL Bioessays 14:105-111(1992).
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT
CC IS CLAMPED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-
CC INDEPENDENT) ALONG DUPLICATION DNA.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA) (N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLII' COMPLEX. POLII' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN. THE FINAL COMPOSITION OF THE
CC COMPLEX IS: (ALPHA,EPSILON,THETA) [2]-TAU[2]-(GAMMA,DELTA,DELTA',
CC PSI,CHI) [2]-BETA[4]. THE BETA CHAIN IS AN HOMODIMER, WHEN NOT
CC ASSOCIATED WITH THE OTHER COMPONENTS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -----
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CC -----
CC EMBL; J01602; AA59150.1; -;
CC EMBL; L10328; AAA62052.1; -;
DR EMBL; AB000447; AAC76724.1; -;
DR EMBL; AB005601; AAG58898.1; -;
DR EMBL; AF002566; BAB38059.1; -;
DR EMBL; M19876; AAA23695.1; -;
DR EMBL; M13822; AAA24512.1; -;
DR EMBL; K02179; AAA24510.1; -;
DR EMBL; X04341; CAA27869.1; -;
DR PIR; B24944; DJEC3B.
DR PIR; A22168; A22168.
DR ECO2DBASE; A036.1; 6TH EDITION.
DR ECO2DBASE; B036.1; 6TH EDITION.
DR EcoGene; EG10242; dnan.
DR InterPro; IPR001001; DNA_polIII_beta.
DR Pfam; PF00712; DNA_pol3_beta_1.
DR Pfam; PF02767; DNA_pol3_beta_2; 1.
DR Pfam; PF02768; DNA_pol3_beta_3; 1.
DR SMART; SM00480; POL3Bc; 1.
DR TIGRFAMS; TIGR00663; dnan; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW 3D-structure; Complete proteome.
FT DOMAIN 1 125 I.
FT DOMAIN 126 253 II.
FT DOMAIN 254 366 III.
FT STRAND 2 6
FT HELIX 7 17
FT TURN 18 18
FT HELIX 28 31
FT STRAND 32 38
FT TURN 39 40
FT STRAND 41 47
FT STRAND 51 58
FT STRAND 64 64
FT STRAND 66 71
FT HELIX 72 81
FT TURN 84 85
FT STRAND 87 93
FT TURN 94 95
FT STRAND 96 101
FT TURN 102 103
FT STRAND 104 109
FT STRAND 111 111
FT HELIX 113 115
FT STRAND 124 130
FT HELIX 132 140
FT TURN 141 142
FT HELIX 143 145
FT HELIX 153 155
FT STRAND 157 172
FT STRAND 176 196
FT HELIX 197 206
FT STRAND 214 219
FT STRAND 222 227
FT TURN 228 229
FT STRAND 230 235
FT HELIX 244 247
FT STRAND 254 259
FT HELIX 260 271
FT TURN 272 273
FT TURN 276 278
FT STRAND 280 286
FT TURN 287 288
FT STRAND 289 295
FT TURN 297 298
FT STRAND 301 307
FT STRAND 309 309
FT STRAND 315 320
FT HELIX 321 330
FT STRAND 335 340
FT TURN 343 344
FT STRAND 347 351
FT TURN 352 353
FT STRAND 354 361

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FT STRAND 364 364
SQ SEQUENCE 366 AA; 40586 MW; 7A45646F61255B5A CRC64;

Query Match 100.0%; Score 23; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 304 EILDV 308

RESULT 26
ID DP3B_SALTY STANDARD; PRT; 366 AA.
AC P26464; OS0240;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase III, beta chain (EC 2.7.7.7).
GN DNAN OR STM3837.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OC NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Amini F., Blinkova A., Walker J.R.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856 (2001).
RN [3]
RP SEQUENCE OF 1-62 FROM N.A.
RX MEDLINE=87307970; PubMed=3040670;
RA Skovgaard O., Hansen F.G.;
RT "Comparison of dnaA nucleotide sequences of Escherichia coli,
RT Salmonella typhimurium, and Serratia marcescens."
RL J. Bacteriol. 169:3976-3981 (1987).
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT
CC IS CLAMPED ONTO DNA, IT SLIDES FREELY (BIDIRECTIONAL AND ATP-
CC INDEPENDENT) ALONG DUPLEX DNA.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}(N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLIII' COMPLEX. POLIII' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN. THE FINAL COMPOSITION OF THE
CC COMPLEX IS: (ALPHA,EPSILON,THETA) [2]-TAU[2]-(GAMMA,DELTA,DELTA',
CC PSI,CHI) [2]-BETA[4].
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC
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CC
DR EMBL; AF034747; AAB87631.1; -.
DR EMBL; AE008879; AAL22696.1; -.
DR EMBL; M17352; AAA02816.1; -.
DR HSP; P00583; 2POL.
DR StyGene; SG10089; dnaN.
DR InterPro; IPR001001; DNA_polIII_beta.
DR Pfam; PF00712; DNA_pol3_beta_1.
DR Pfam; PF02767; DNA_pol3_beta_2; 1.
DR Pfam; PF02768; DNA_pol3_beta_3; 1.
DR SMART; SM00480; POL3BG; 1.
DR TIGRFAMs; TIGR00663; dnan; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.
FT CONFLICT 41 T -> A (IN REF. 3).
SQ SEQUENCE 366 AA; 40548 MW; 575FD8F13D928742 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 304 EILDV 308

RESULT 27
P37 MYCPN
ID P37_MYCPN STANDARD; PRT; 380 AA.
AC P75371;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE High affinity transport system protein P37 precursor.
GN P37 OR WPN415 OR WP425.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449 (1996).
CC -1- FUNCTION: P37 IS PART OF A HIGH-AFFINITY TRANSPORT SYSTEM.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor.
CC
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CC
DR EMBL; AB000041; AAB96073.1; -.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Transport; Membrane; Lipoprotein; Signal; Complete proteome.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 380 HIGH AFFINITY TRANSPORT SYSTEM PROTEIN
P37.
FT LIPID 27 27 N-ACYL DIGLYCERIDE (PROBABLE).
SQ SEQUENCE 380 AA; 43495 MW; B8EBDE2199CC792 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 304 EILDV 308
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Db 370 EILDV 374
RESULT 28
RPA2_ARCFU
ID _RPA2_ARCFU STANDARD; PRT; 380 AA.
AC 029350;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase subunit A" (EC 2.7.7.6).
GN RPA2 OR AF1889.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA] (N).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC
CC EMBL; AB000972; AAB89364.1; -
CC TIGR; AF1889; -
CC InterPro; IPR002879; RNA_pol_A2.
CC Pfam; PF01854; RNA_pol_A2; 1
CC Transferrase; Transcription; DNA-directed RNA polymerase;
CC Complete proteome.
CC SEQUENCE 380 AA; 42422 MW; 84EA204F7B0BCEB6 CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 380;
CC Best Local Similarity 100.0%; Pred. No. 2e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC 1 EILDV 5
CC |||||
CC 98 EILDV 102
CC
RESULT 29
YXEP_BACSU
ID _YXEP_BACSU STANDARD; PRT; 380 AA.
AC P54955;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE Hypothetical protein yxep.
GN YXEP OR LP98.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / BGSC1A1;
RX MEDLINE=97021444; PubMed=8867804;
RA Yoshida K.-I., Fujimura M., Yanai N., Fujita Y.;
RT "Cloning and sequencing of a 23-kb region of the Bacillus subtilis
RT genome between the iol and hut operons."
RL DNA Res. 2:295-301(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Møller I., Albertini A.M., Alloni G.,
RA Azevedo V., Berto M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschii C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,
RA Denizot P., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Haeche J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.P., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Ruchle E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S.,
RA Sorokin A., Taconelli E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis."
RL Nature 390:249-256(1997).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M40.
CC
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CC
CC EMBL; D45912; BAA08332.1; -
CC EMBL; Z99124; CAB15983.1; -
CC MEROPS; M40.UPW; -
CC Subtilisin, BG11892; Yxep.
CC InterPro; IPR002933; Peptidase_M20.
CC Pfam; PF01546; Peptidase_M20; 1
CC Hypothetical protein; Hydrolase; Complete proteome.
CC SEQUENCE 380 AA; 41596 MW; BD145964FAE42118 CRC64;
CC
CC Query Match 100.0%; Score 23; DB 1; Length 380;
CC Best Local Similarity 100.0%; Pred. No. 2e+02;
CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC 1 EILDV 5
CC |||||

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Db 44 EILDV 48

RESULT 30
2ASE MOUSE
ID 2ASE_MOUSE STANDARD; PRT; 387 AA.
AC Q61151;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE epsilon isoform (PP2A, B subunit, B' epsilon isoform) (PP2A, B
DE subunit, B56 epsilon isoform) (PP2A, B subunit, Pp61 epsilon isoform)
DE (PP2A, B subunit, R5 epsilon isoform) (Fragment).
DE PP2R5E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=97042488; PubMed=8887688;
RA Okamoto K., Kamibayashi C., Serrano M., Prives C., Mumby M.C.,
RA Beach D.;
RT "p53-dependent association between cyclin G and the B' subunit of
RT protein phosphatase 2A.";
RL Mol. Cell. Biol. 16:6593-6602 (1996).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT.
RA Hulo C.;
RL Unpublished observations (JAN-2000).
CC -!- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
CC COMPARTMENT. INTERACTS WITH CYCLIN G (IN VITRO).
CC -!- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
CC COMPOSED OF A 35 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CC CONSTANT REGULATORY SUBUNIT (Pp65 OR SUBUNIT A), THAT ASSOCIATES
CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
CC B (THE R2/B/PR55/B55, R3/B'/PR72/PR130/PR59 AND R5/B'/B56
CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
CC AND CELL SIGNALING MOLECULES.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
CC FAMILY.
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
CC INTRODUCED FROM POSITION 112-135 TO EXTEND THE SIMILARITY WITH THE
CC HUMAN HOMOLOG.
CC -----
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CC -----
CC EMBL; U49728; AAB37234.1; ALT_FRAME.
CC MGD; MGI:1349473; Pp2r5e.
CC InterPro; IPR002554; B56.
CC Pfam; PF01603; B56; 1.
CC Multigene family.
CC FT NON TER 1
CC FT NON TER 387 387
CC SEQUENCE 387 AA; 45497 MW; 780D5404848A548E CRC64;

Query Match 100.0%; Score 23; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 387 387

RESULT 32
YAFI ECOLI
ID YAFI_ECOLI STANDARD; PRT; 414 AA.
AC P04335; P77413;
DT 20-MAR-1987 (Rel. 04, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yafA.

Query Match 100.0%; Score 23; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 390 EILDV 394

RESULT 31
CEGT HUMAN
ID CEGT_HUMAN STANDARD; PRT; 394 AA.
AC Q16739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ceramide glucosyltransferase (EC 2.4.1.80) (Glucosylceramide synthase)
DE (GCS) (UDP-glucose:N-acylsphingosine D-glucosyltransferase) (GLCT-1).
DE USCG.
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96209784; PubMed=8643456;
RA Ichikawa S., Sakiyama H., Suzuki G., Hidari K.I.-P., Hirabayashi Y.;
RT "Expression cloning of a cDNA for human ceramide glucosyltransferase
RT that catalyzes the first glycosylation step of glycosphingolipid
RT synthesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:4638-4643 (1996).
CC -!- FUNCTION: MAY SERVE AS "FLIPPASE" AS WELL AS A GLUCOSYLTRANSFERASE
CC THAT TRANSFERS GLUCOSE TO CERAMIDE.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + N-acylsphingosine = UDP + D-
CC glucosyl-N-acylsphingosine.
CC -!- PATHWAY: FIRST GLYCOSYLATION STEP OF GLYCOSPHINGOLIPID SYNTHESIS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum.
CC -!- TISSUE SPECIFICITY: FOUND IN ALL TISSUES EXAMINED.
CC -----
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CC -----
CC EMBL; D50840; BAA09451.1; -.
CC Genbank; HGNC:12524; UGCG.
CC MIM; 602874; -.
CC InterPro; IPR001173; Glycos transf 2.
CC Pfam; PF00535; Glycos transf 2; 1.
CC Transmem; Glycosyltransferase; Transmembrane; Signal-anchor;
CC Endoplasmic reticulum.
CC DOMAIN 1 10 LUMENAL (POTENTIAL).
CC FT TRANSMEM 11 31 SIGNAL-ANCHOR (POTENTIAL).
CC FT TRANSMEM 286 306 POTENTIAL.
CC FT TRANSMEM 314 334 POTENTIAL.
CC SEQUENCE 394 AA; 44853 MW; 3B958569F8A96449 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 390 EILDV 394
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GN YAJA OR B0239.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85155481; PubMed=6397401;
RA Nuesch J., Schumperli D.;
RT "Structural and functional organization of the gpt gene region of
RL Escherichia coli.";
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / W3110;
RA Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,
RA Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
RA Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RL 4.0 - 6.0 min (189,987 - 281,416bp) region.";
RN [4]
RP Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
RA Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
RA Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
RA Davis R.W.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN
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CC -----
DR EMBL; M13422; AAA23929.1; -.
DR EMBL; AE000132; AAC73343.1; -.
DR EMBL; D83536; BAA77908.1; -.
DR EMBL; U70214; AAB08659.1; -.
DR PIR; A04451; Q0EC49.
DR EcoGene; EGI1091; yafa.
DR InterPro; IPR000379; Ser_estrs_site.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 242 242 T -> S (IN REF. 1 AND 3).
FT CONFLICT 277 278 NV -> TL (IN REF. 1 AND 3).
FT CONFLICT 397 414 NFDGLQIETDWIEKRLC -> KILTKVERSPGSKNACV
FT KNILFANLVQLHNR (IN REF. 1 AND 3).
SQ SEQUENCE 414 AA; 47008 MW; 2C154E46CFC9565E CRC64;

Query Match 100.0%; Score 23; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 65 EILDV 69

RESULT 33
YAJA SALTY
ID YAJA_SALTY STANDARD; PRT; 414 AA.

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AC P37722;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yafa.
GN YAJA OR STM0318.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Lf2 / SGSC1412 / ATCC 700720;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL Lf2.";
RN [2]
RP Nature 413:852-856(2001).
RX STRAIN=Lf2 / SGSC1412 / ATCC 700720;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RL Lf2.";
RN [3]
RP Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP IDENTIFICATION
RX MEDLINE=95004589; PubMed=7920643;
RA Robison K., Gilbert W., Church G.M.;
RT "Large scale bacterial gene discovery by similarity search.";
RL Nat. Genet. 7:205-214(1994).
RN
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE008709; AAL19274.1; -.
DR EMBL; X63336; -. NOT ANNOTATED_CDS.
DR StvGene; SG10415; Yafa.
DR InterPro; IPR000379; Ser_estrs_aite.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 28 30 NRG -> IV (IN REF. 2).
FT CONFLICT 35 36 MQ -> CI (IN REF. 2).
SQ SEQUENCE 414 AA; 47159 MW; B0B2843A26B263D1 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 65 EILDV 69

RESULT 34
2A5G MOUSE
ID 2A5G_MOUSE STANDARD; PRT; 435 AA.
AC Q60956; Q35708;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B
DE B56 gamma isoform) (PP2A, B subunit, PR61 gamma isoform) (PP2A, B
DE subunit, R5 gamma isoform) (PP2A, B subunit, B' alpha3 isoform)
DE (Fragment).
GN PPP2R5C.

```

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX TISSUE=T-cell;
RC MEDLINE=96214950; PubMed=8617797;
RA Tehrani M.A., Mumby M.C., Kamibayashi C.;
RT "Identification of a novel protein phosphatase 2A regulatory subunit
highly expressed in muscle.";
RL J. Biol. Chem. 271:5164-5170(1996).
RN (2)
RP SEQUENCE OF 15-435 FROM N.A.
RC STRAIN=CS7BL/6;
RX MEDLINE=96354596; PubMed=8752144;
RA Francia G., Mitchell S.D., Moss S.E., Hanby A.M., Marshall J.F.,
Hart I.R.;
RT "Identification by differential display of annexin-VI, a gene
differentially expressed during melanoma progression.";
RL Cancer Res. 56:3855-3858(1996).
CC -1- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
COMPARTMENT. INTERACTS WITH CYCLIN G IN VITRO.
CC -1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, LIVER AND BRAIN. LOWER
LEVELS IN SKELETAL MUSCLE, SPLEEN, KIDNEY, AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
FAMILY.

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DR EMBL; U37353; AAC52435.1; -;
DR EMBL; U59418; AAB70857.1; -;
DR MGD; MGI:1349475; Ppp2r5c.
DR InterPro; IPR002554; B56.
DR Pfam; PF01603; B56; 1.
KW Multigene family.
FT NON TER 1
FT CONFLICT 15 15 D -> N (IN REF. 2).
SQ SEQUENCE 435 AA; 51196 MW; E3C2DF4C57F729C2 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 293 EILDV 297
|||||
RESULT 35
2ASE HUMAN
ID _2ASE_HUMAN STANDARD; PRT; 467 AA.
AC Q16537;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE epsilon isoform (PP2A, B subunit, B' epsilon isoform) (PP2A, B
DE subunit, B56 epsilon isoform) (PP2A, B subunit, PR61 epsilon isoform)
DE (PP2A, B subunit, R5 epsilon isoform).
GN PPP2R5E.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A., AND SEQUENCE OF 449-455.
RC TISSUE=Fetal retina;
RX MEDLINE=96276417; PubMed=8694763;
RA Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
Merlevede W., Goris J., Hemmings B.A.;
RT "The variable subunit associated with protein phosphatase 2A0 defines
a novel multimer family of regulatory subunits.";
RL Biochem. J. 317:187-194(1996).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=96355607; PubMed=8703017;
RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;
RT "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits
encodes differentiation-induced phosphoproteins that target PP2A to
both nucleus and cytoplasm.";
RL J. Biol. Chem. 271:22081-22089(1996).
CC -1- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
COMPARTMENT.
CC -1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
FAMILY.

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DR EMBL; Z69029; CAA93153.1; -;
DR EMBL; L76703; AAB69752.1; -;
DR Genew; HGNC:9313; PPP2R5E.
DR MIM; 601647; -;
DR InterPro; IPR002554; B56.
DR Pfam; PF01603; B56; 1.
KW Phosphorylation; Multigene family.
SQ SEQUENCE 467 AA; 54699 MW; DD9CE11433F499CF CRC64;

Query Match 100.0%; Score 23; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 327 EILDV 331
|||||
RESULT 36
YAPI_MOUSE
ID _YAPI_MOUSE STANDARD; PRT; 472 AA.

P46938;
 01-NOV-1995 (Rel. 32, Created)
 01-NOV-1995 (Rel. 32, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 65 kDa Yes-associated protein (YAP65).
 YAP1 OR YAP65 OR YAP.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 STRAIN=NIH Swiss; TISSUE=Embryo;
 MEDLINE=95301570; PubMed=7782338;
 Sudol M., Bork P., Einbond A., Kastury K., Druck T., Negrini M.,
 Huebner K., Lehman D.;
 "Characterization of the mammalian YAP (Yes-associated protein) gene
 and its role in defining a novel protein module, the WW domain.";
 J. Biol. Chem. 270:14733-14741(1995).
 CC -1- FUNCTION: BINDS TO THE SH3 DOMAIN OF THE YES KINASE
 (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 WW DOMAINS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X80508; CAA56673.1; -;
 DR MGD; MGI:103262; YAP.
 DR InterPro; IPR002349; WW.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR Pfam; PF00397; WW; 2.
 DR PRINTS; PR00403; WWDOMAIN.
 DR SMART; SM00456; WW; 2.
 DR PROSITE; PS01159; WW DOMAIN 1; 2.
 DR PROSITE; PS00020; WW DOMAIN 2; 2.
 KW Phosphorylation; Repeat.
 FT DOMAIN 156 189 WW 1.
 FT DOMAIN 215 248 WW 2.
 SQ SEQUENCE 472 AA; 50703 MW; 174FD33E0381126C CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 472;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 450 EILDV 454
 RESULT 37
 DCOR NEUCR
 ID DCOR NEUCR STANDARD; PRT; 484 AA.
 AC P27121;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Ornithine decarboxylase (EC 4.1.1.17) (ODC).
 GN SPE-1.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OC NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ST. LAWRENCE 74 / SL 74 / ORS 6A;
 RA MEDLINE=92107187; PubMed=1530878;
 RW Williams L.J., Barnett G.R., Ristow J.L., Pitkin J., Perriere M.,

Davis R.H.;
 "Ornithine decarboxylase gene of Neurospora crassa: isolation,
 sequence, and polyamine-mediated regulation of its mRNA.";
 Mol. Cell. Biol. 12:347-359(1992).
 CC -1- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- ENZYME REGULATION: ODC SYNTHESIS IS ENHANCED POSTTRANSCRIPTIONALLY
 BY AN EXCESS OF PUTRESCINE. THIS POLYAMINE-MEDIATED CONTROL IS
 UNIQUE TO N. CRASSA.
 CC -1- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY
 OF POLYAMINE BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine
 DECARBOXYLASES.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-3 IS THE INITIATOR.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M68969; AAA33604.1; -;
 DR EMBL; M68970; AAA33605.1; -;
 DR EMBL; L16920; AAA33614.1; -;
 DR PIR; A42065; A42065.
 DR HGSP; P07805; IP3T.
 DR InterPro; IPR000183; Decarboxylase2.
 DR Pfam; PF00218; Orn_DAP_Arg_dec; 1.
 DR Pfam; PF02784; Orn_Arg_dec_N; 1.
 DR PRINTS; PR01179; ODADCBXKLASE.
 DR PROSITE; PS00878; ODR_DC_2_1; 1.
 DR PROSITE; PS00879; ODR_DC_2_2; 1.
 KW Lyase; Decarboxylase; Pyridoxal phosphate; Polyamine biosynthesis.
 FT BINDING 114 442 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT ACT_SITE 422 422 BY SIMILARITY.
 SQ SEQUENCE 484 AA; 53300 MW; 3554F4315EA44A6P CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 484;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 436 EILDV 440
 RESULT 38
 2A5A HUMAN
 ID 2A5A HUMAN STANDARD; PRT; 486 AA.
 AC Q15172;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
 DE alpha isoform (pp2A, B subunit, B' alpha isoform) (pp2A, B subunit,
 DE B56 alpha isoform) (pp2A, B subunit, pp61 alpha isoform) (pp2A, B
 DE subunit, R5 alpha isoform).
 GN PP2R5A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast cancer;
 RX MEDLINE=96064678; PubMed=7592815;
 RA McCright B., Virshup D.M.;
 RT "Identification of a new family of protein phosphatase 2A regulatory
 subunits.";
 RL J. Biol. Chem. 270:26123-26128(1995).
 RN [2]

RP SEQUENCE OF 47-56; 129-132; 347-354; 448-462 AND 471-480.
RC TISSUE=Brain;
RX MEDLINE=96276417; PubMed=9694763;
RA Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
RA Merlevede W., Goris J., Hemmings B.A.;
RT "The variable subunit associated with protein phosphatase 2A0 defines
RT a novel multimer family of regulatory subunits.";
RL Biochem. J. 317:187-194 (1996).
RN [3]
RP PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
RX MEDLINE=96355607; PubMed=8703017;
RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;
RA "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits
RT encodes differentiation-induced phosphoproteins that target PP2A to
RT both nucleus and cytoplasm.";
RL J. Biol. Chem. 271:22081-22089 (1996).
CC -1- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
CC COMPARTMENT.
CC -1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
CC COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CC CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
CC B (THE R2/B/PR55/B55, R3/B'/PR72/PR130/PR59 AND R5/B'/B56
CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
CC AND CELL SIGNALING MOLECULES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH THE HIGHEST EXPRESSION
CC IN HEART AND SKELETAL MUSCLE.
CC -1- PTM: PHOSPHORYLATED ON SERINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
CC FAMILY.

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DR EMBL; L42373; AAC37601.1; -;
DR Genew; HGNC:9309; PPT2R5A.
DR MIM; 601643; -;
DR InterPro; IPR002554; B56.
DR Pfam; PF01603; B56; 1.
DR Phosphorylation; Multigene family.
KW DOMAIN 2 5 POLY-SER.
FT CONFLICT 52 52 E -> F (IN REF. 2; AA SEQUENCE).
FT CONFLICT 54 54 H -> S (IN REF. 2; AA SEQUENCE).
FT CONFLICT 451 451 R -> E (IN REF. 2; AA SEQUENCE).
SQ SEQUENCE 486 AA; 56193 MW; D31407F7032A6D44 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 335 EILDV 339
|||||
RESULT 39
PYR5 DROME
ID PYR5 DROME STANDARD; PRT; 493 AA.
AC Q01637; Q24221;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Uridine 5'-monophosphate synthase (UMP synthase) (Rudimentary-like
DE protein) [includes: Orotate phosphoribosyltransferase (EC 2.4.2.10)

DE (OPRase); Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
DE (OMPdecase)}.
GN R-L.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
OX [1]
RN SEQUENCE FROM N.A.
RP Eisenberg M.T., Kirkpatrick R., Rawls J.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=91042409; PubMed=2122228;
RA Eisenberg M.T., Gathy K., Vincent T., Rawls J.;
RT "Molecular cloning of the UMP synthase gene rudimentary-like from
RT Drosophila melanogaster.";
RL Mol. Gen. Genet. 222:1-8 (1990).
CC -1- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate = orotate
CC + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -1- PATHWAY: Pyrimidine biosynthesis; Orotidine 5'-phosphate = UMP + CO(2).
CC -1- PATHWAY: Pyrimidine biosynthesis; fifth and sixth (last) steps.
CC -1- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE
CC PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
CC OMP DECARBOXYLASE FAMILY.

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DR EMBL; L00968; AAA29012.1; -;
DR EMBL; X54230; CAA38138.1; -;
DR PIR; S11907; S11907.
DR HSP; P03962; IDQW.
DR FlyBase; FBgn0003257; r-1.
DR InterPro; IPR001754; OMPdecase.
DR InterPro; IPR000836; PRTtransferase.
DR InterPro; IPR002375; Pr/PY-TP_transf.
DR InterPro; IPR004467; Pyre.
DR Pfam; PF00156; Pribosyltran; 1.
DR Pfam; PF00215; OMPdecase; 1.
DR TIGRFAMs; TIGR00336; pyre; 1.
DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
DR PROSITE; PS00156; OMPDECASE; 1.
KW Pyrimidine biosynthesis; Multifunctional enzyme; Transferase;
KW Glycosyltransferase; Lyase; Decarboxylase.
FT DOMAIN 1 207 OPRASE.
FT DOMAIN 208 233 DOMAIN LINKER.
FT DOMAIN 234 493 OMPDECASE.
FT ACT SITE 320 320 BY SIMILARITY.
FT CONFLICT 47 51 LGLPQ -> YPDWM (IN REF. 2).
SQ SEQUENCE 493 AA; 53327 MW; 56479CDAB1F6A308 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 493;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 271 EILDV 275
|||||
RESULT 40
2ASB HUMAN
ID 2ASB HUMAN STANDARD; PRT; 497 AA.
AC Q15173; Q13853;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE beta isoform (PP2A, B subunit, B' beta isoform) (PP2A, B subunit,
DE B56 beta isoform) (PP2A, B subunit, PR61 beta isoform) (PP2A, B
DE subunit, R5 beta isoform).
GN PPR2R5B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA-1).
RC TISSUE=Fetal brain;
RX MEDLINE=9606478; PubMed=7592815;
RA McCright B., Virshup D.M.;
RT "Identification of a new family of protein phosphatase 2A regulatory
RT subunits";
RN J. Biol. Chem. 270:26123-26128(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA-2), AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=96276417; PubMed=8694763;
RA Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
RA Merlievede W., Goris J., Hemmings B.A.;
RT "The variable subunit associated with protein phosphatase 2A defines
RT a novel multimer family of regulatory subunits";
RN Biochem. J. 317:187-194(1996).
RN [3]
RP PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
RX MEDLINE=96355607; PubMed=8703017;
RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;
RA "The B56 family of protein phosphatase 2A (pp2A) regulatory subunits
RT encodes differentiation-induced phosphoproteins that target PP2A to
RT both nucleus and cytoplasm";
RN J. Biol. Chem. 271:22081-22089(1996).
CC [1]- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
CC COMPARTMENT.
CC [1]- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
CC COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CC CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
CC B (THE R2/B/PR55/B55, R3/B'/PR72/PR130/PR59 AND R5/B'/B56
CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
CC AND CELL SIGNALING MOLECULES.
CC [1]- SUBCELLULAR LOCATION: Cytoplasmic.
CC [1]- ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-1 (SHOWN HERE) AND BETA-2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC [1]- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BRAIN.
CC [1]- INDUCTION: BY RETINOIC ACID; IN NEUROBLASTOMA CELL LINES.
CC [1]- PTM: AT LEAST ISOFORM BETA-1 IS PHOSPHORYLATED ON SERINE RESIDUES.
CC [1]- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; L42374; AAC37602.1; -;
CC EMBL; Z69028; CRA93152.1; -;
CC Genbank; HGNC:9310; PPR2R5B.
CC MIM; 601644; -;
CC InterPro; IPR002554; B56.
CC Pfam; PF01603; B56; 1.
CC Phosphorylation; Alternative splicing; Multigene family.
CC VARSPLIC 1 19 METKLPPASTTSPSSPGL -> MITVNPPLPQDTVNLF

FT CONFLICT 57 58 (IN ISOFORM BETA-2).
FT CONFLICT 177 178 QE -> IF (IN REF. 2; AA SEQUENCE).
FT CONFLICT 181 181 ES -> GA (IN REF. 2; AA SEQUENCE).
FT CONFLICT 184 184 F -> M (IN REF. 2; AA SEQUENCE).
FT CONFLICT 461 461 S -> M (IN REF. 2; AA SEQUENCE).
SQ SEQUENCE 497 AA; 57393 MW; 8BEF84F20A77982D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 341 BILDV 345
|||||

RESULT 41
2ASB RABIT STANDARD; PRT; 500 AA.
AC Q28647;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE beta isoform (PP2A, B subunit, B' beta isoform) (PP2A, B subunit,
DE B56 beta isoform) (PP2A, B subunit, PR61 beta isoform) (PP2A, B
DE subunit, R5 beta isoform) (PP2A, B subunit, B'-alpha).
GN PPR2R5B.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand;
RX MEDLINE=9616194; PubMed=8576224;
RA Scioros C., Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
RT "High complexity in the expression of the B' subunit of protein
RT phosphatase 2A0. Evidence for the existence of at least seven novel
RT isoforms";
RN J. Biol. Chem. 271:2578-2588(1996).
CC [1]- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
CC COMPARTMENT.
CC [1]- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
CC COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CC CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
CC B (THE R2/B/PR55/B55, R3/B'/PR72/PR130/PR59 AND R5/B'/B56
CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
CC AND CELL SIGNALING MOLECULES.
CC [1]- SUBCELLULAR LOCATION: Nuclear (by similarity).
CC [1]- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC [1]- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
CC FAMILY.
CC [1]- CAUTION: NOMENCLATURE USED IN REF.1 REFERS TO PP2A B SUBUNIT
CC B' ALPHA ISOFORM, WHICH IS CITED AS PP2A B SUBUNIT BETA-PR61
CC ISOFORM IN LATER PUBLICATIONS.
CC
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CC
CC EMBL; U37769; AAC48527.1; -;
CC InterPro; IPR002554; B56.
CC Pfam; PF01603; B56; 1.
CC

KW Multigene family; Nuclear protein.
SQ SEQUENCE 500 AA; 57709 MW; 001CA9360E4C04B0 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
Db 341 EILDV 345
RESULT 42
GLPK_PSETO STANDARD; PRT; 503 AA.
AC 087924;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE GlyceroL kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK).
GN GLPK.
OS Pseudomonas tolaasii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=29442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PT814;
RA Murata H.;
RT "GlpK of Pseudomonas tolaasii.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: KEY ENZYME IN THE REGULATION OF GLYCEROL UPTAKE AND METABOLISM.
CC -!- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
CC -!- PATHWAY: Glycerol utilization; rate-limiting step.
CC -!- SIMILARITY: BELONGS TO THE FUCOKINASE / GLUCOKINASE / GLYCEROKINASE / XYLULOXINASE FAMILY.

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DR EMBL; AB015974; BAA31995.1; -.
DR HSSP; P08859; 1GLC.
DR InterPro; IPR000577; FGGY_kin.
DR Pfam; PF00370; FGGY; 1.
DR Pfam; PF02782; FGGY_C; 1.
DR TIGRFAMs; TIGR01311; glycerol kin; 1.
DR PROSITE; PS00445; FGGY_KINASES 2; 1.
DR PROSITE; PS00933; FGGY_KINASES 1; 1.
KW Glycerol metabolism; Transferase; Kinase; ATP-binding.
FT NP_BIND 160 172 ATP (POTENTIAL).
SQ SEQUENCE 503 AA; 55768 MW; 928BEFCC5462C8CE CRC64;
Query Match 100.0%; Score 23; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
Db 211 EILDV 215
RESULT 43
SYG_DEIRA STANDARD; PRT; 506 AA.
AC Q9RSR5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS).
DE GlyRS OR DR2059.
GN GLYS OR DR2059.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O.; Eisen J.A.; Heidelberg J.F.; Hickey E.K.; Peterson J.D.; Dodson R.J.; Haft D.H.; Gwinn M.L.; Nelson W.C.; Richardson D.L.; Moffat K.S.; Qin H.; Jiang L.; Pamphile W.; Crosby M.; Shen M.; Vamathevan J.J.; Lam P.; McDonald L.; Utterback T.; Zaleski C.; Makarova K.S.; Aravind L.; Daly M.J.; Minton K.W.; Fleischmann R.D.; Ketchum K.A.; Nelson K.E.; Salzberg S.; Smith H.O.; Venter J.C.; Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI.";
RL Science 286:1571-1577(1999).
CC -!- CATALYTIC ACTIVITY: ATP + glycine + tRNA (Gly) = AMP + diphosphate + glycyl-tRNA (Gly).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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DR EMBL; AE002042; AAF11606.1; ALT_INIT.
DR HSSP; P56206; IAT1.
DR TIGR; DR2059; -.
DR InterPro; IPR002106; AatRNA_ligaseII.
DR InterPro; IPR004154; HGTP anticodon.
DR InterPro; IPR002314; tRNA-synt 2b.
DR InterPro; IPR002315; tRNA-synt_gly.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR Pfam; PF03129; HGTP anticodon; 1.
DR PRINTS; PR01043; TRNASYNTHGLY.
DR TIGRFAMs; TIGR00389; glyS dimeric; 1.
DR PROSITE; PS50862; AA TRNA_LIGASE II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding; Complete proteome.
SQ SEQUENCE 506 AA; 57204 MW; 23A7C69DE83D2D01 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
Db 276 EILDV 280
RESULT 44
FINC_CANFA STANDARD; PRT; 522 AA.
AC Q28275; Q28276;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibronectin (FN) (fragment).
GN FN1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.

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OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT (V+C)-.
RC TISSUE=Cartilage;
RX MEDLINE=96324983; PubMed=8702559;
RA Macleod J.N., Burton-Wurster N., Gu D.N., Lust G.;
RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
RL encoding the V, III-15, and I-10 protein segments.";
RJ J. Biol. Chem. 271:18954-18960(1996).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX
CC ORGANIZATION OF CARTILAGE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING. VARIANT
CC (V+C)- LACKS REPEAT 15 OF FIBRONECTIN TYPE-III, REPEAT 10 OF
CC FIBRONECTIN TYPE-I, AND THE CONNECTING STRAND 3.
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX. VARIANT (V+C)-
CC IS THE MAJOR TRANSCRIPT IN ARTICULAR CARTILAGE, BUT IT IS ABSENT
CC FROM LIVER.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS AT LEAST 4 FIBRONECTIN TYPE III DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 3 FIBRONECTIN TYPE I DOMAINS.
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CC -----
DR ENBL; U52106; AAC48612.1; -.
DR ENBL; U52105; AAC48611.1; -.
DR HSSP; P02751; IFNH.
DR InterPro; IPR003961; FN III.
DR Pfam; PF00039; fn1; 3.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00060; FN3; 3.
DR PROSITE; PS01253; FIBRONECTIN 1; 2.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KW Repeat; Sulfation; Alternative splicing.
FT NON_TER 1
FT DOMAIN <1 204
FT HEPARIN-BINDING 2 (BY SIMILARITY).
FT DOMAIN 325 >522
FT FIBRIN-BINDING 2 (BY SIMILARITY).
FT DOMAIN <1 25
FT FIBRONECTIN TYPE-III 13.
FT DOMAIN 26 114
FT FIBRONECTIN TYPE-III 14.
FT DOMAIN 115 204
FT FIBRONECTIN TYPE-III 15.
FT DOMAIN 205 315
FT CONNECTING STRAND 3 (CS-3) (V REGION).
FT DOMAIN 316 395
FT FIBRONECTIN TYPE-III 16.
FT DOMAIN 417 461
FT FIBRONECTIN TYPE-I 10.
FT DOMAIN 462 504
FT FIBRONECTIN TYPE-I 11.
FT DOMAIN 506 >522
FT FIBRONECTIN TYPE-I 12.
FT SITE 304 306
FT CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 419 448
FT BY SIMILARITY.
FT DISULFID 446 458
FT BY SIMILARITY.
FT DISULFID 464 491
FT BY SIMILARITY.
FT DISULFID 489 501
FT BY SIMILARITY.
FT DISULFID 508 >522
FT MOD RES 509 509
FT SULFATION (POTENTIAL).
FT CARBOHYD 321 321
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 205 205
FT D -> E (IN ISOFORM (V+C)-).

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FT VARSPLIC 206 462 MISSING (IN ISOFORM (V+C)-).
FT NON_TER 522
SQ SEQUENCE 522 AA; 57700 MW; DB1D9A54C2BDAE26 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 222 EILDV 226

RESULT 45
FINC HORSE
ID FINC HORSE STANDARD; PRT; 522 AA.
AC Q28377; Q28378;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibronectin (FN) (Fragment).
GN FN1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96324983; PubMed=8702559;
RA Macleod J.N., Burton-Wurster N., Gu D.N., Lust G.;
RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
RL encoding the V, III-15, and I-10 protein segments.";
RJ J. Biol. Chem. 271:18954-18960(1996).
CC -1- FUNCTION: FIBRONECTINS BIND CELL SURFACES AND VARIOUS COMPOUNDS
CC INCLUDING COLLAGEN, FIBRIN, HEPARIN, DNA, AND ACTIN. FIBRONECTINS
CC ARE INVOLVED IN CELL ADHESION, CELL MOTILITY, OPSONIZATION, WOUND
CC HEALING, AND MAINTENANCE OF CELL SHAPE.
CC -1- FUNCTION: VARIANT (V+C)- IS PROBABLY INVOLVED IN MATRIX
CC ORGANIZATION OF CARTILAGE.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- ALTERNATIVE PRODUCTS: EACH OF THE "EXTRA DOMAIN" & THE CONNECTING
CC STRAND 3 ARE PRESENT IN SOME FORMS OF FIBRONECTIN AND ABSENT IN
CC OTHERS. THESE DIFFERENCES ARE DUE TO ALTERNATIVE SPLICING. VARIANT
CC (V+C)- LACKS REPEAT 15 OF FIBRONECTIN TYPE-III, REPEAT 10 OF
CC FIBRONECTIN TYPE-I, AND THE CONNECTING STRAND 3.
CC -1- TISSUE SPECIFICITY: PLASMA FN (SOLUBLE DIMERIC FORM) IS SECRETED
CC BY HEPATOCYTES. CELLULAR FN (DIMERIC OR CROSS-LINKED MULTIMERIC
CC FORMS), MADE BY FIBROBLASTS, EPITHELIAL AND OTHER CELL TYPES, IS
CC DEPOSITED AS FIBRILS IN THE EXTRACELLULAR MATRIX. VARIANT (V+C)-
CC IS THE MAJOR TRANSCRIPT IN ARTICULAR CARTILAGE, BUT IT IS ABSENT
CC FROM LIVER.
CC -1- PTM: SULFATED (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS AT LEAST 4 FIBRONECTIN TYPE III DOMAINS.
CC -1- SIMILARITY: CONTAINS AT LEAST 3 FIBRONECTIN TYPE I DOMAINS.
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CC -----
DR ENBL; U52107; AAC48613.1; -.
DR ENBL; U52108; AAC48614.1; -.
DR HSSP; P02751; IFNH.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR000083; Fibrctn1.

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DR Pfam; PF00039; fn1; 3.
DR Pfam; PF00041; fn3; 3.
DR SMART; SM00058; FN1; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01253; FIBRONECTIN 1; 2.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
KW Repeat; Sulfation; Alternative splicing.
FT NON TER 1
FT DOMAIN 1 204
FT DOMAIN 325 >522
FT DOMAIN 1 25
FT DOMAIN 26 114
FT DOMAIN 115 204
FT DOMAIN 205 315
FT DOMAIN 316 395
FT DOMAIN 417 461
FT DOMAIN 462 504
FT DOMAIN 506 >522
FT SITE 304 306
FT DISULFID 419 448
FT DISULFID 446 458
FT DISULFID 464 491
FT DISULFID 489 501
FT CARBOHYD 321 321
FT VARSPLIC 205 205
FT VARSPLIC 206 462
FT NON TER 522
SQ SEQUENCE 522 AA; 57577 MW; 893B9AC95864D41 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 222 BILDV 226

RESULT 46
2ASG_HUMAN
ID 2ASG_HUMAN STANDARD; PRT; 524 AA.
AC Q13362; Q14391; Q15174; Q15060;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit,
DE B56 gamma isoform) (PP2A, B subunit, PR61 gamma isoform) (PP2A, B
DE subunit, R5 gamma isoform).
GN PP2R5C OR KIAA0044.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA-3).
RC TISSUE=Umbilical vein;
RX MEDLINE=96214950; PubMed=8617797;
RA Tehrani M.A., Mumby M.C., Kamibayashi C.;
RT "Identification of a novel protein phosphatase 2A regulatory subunit
RT highly expressed in muscle."
RL J. Biol. Chem. 271:5164-5170(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA-1).
RC TISSUE=Fetal retina;
RX MEDLINE=96276417; PubMed=8694763;
RA Zolnierowicz S., van Hoof C., Andjelkovic N., Cron P., Stevens I.,
RA Merlevede W., Goris J., Hemmings B.A.;
RT "The variable subunit associated with protein phosphatase 2A0 defines
RT a novel multimer family of regulatory subunits."
RL Biochem. J. 317:187-194(1996).
RN [3]
RP SEQUENCE OF 2-524 FROM N.A. (ISOFORM GAMMA-2).

RC TISSUE=Bone marrow;
RX MEDLINE=96051398; PubMed=7584044;
RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,
RA Seki N., Kawabayashi Y., Iihikawa K.-I., Tabata S.;
RT "Prediction of the coding sequences of unidentified human genes. II.
RT The coding sequences of 40 new genes (KIAA0041-KIAA0080) deduced by
RT analysis of cDNA clones from human cell line KG-1."
RL DNA Res. 1:223-229(1994).
RN [4]
RP SEQUENCE OF 11-524 FROM N.A. (ISOFORM GAMMA-1).
RX MEDLINE=96064678; PubMed=7592815;
RA McCright B., Virshup D.M.;
RT "Identification of a new family of protein phosphatase 2A regulatory
RT subunits."
RL J. Biol. Chem. 270:26123-26128(1995).
RN [5]
RP PHOSPHORYLATION, AND SUBCELLULAR LOCATION.
RX MEDLINE=96355607; PubMed=8703017;
RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;
RT "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits
RT encodes differentiation-induced phosphoproteins that target PP2A to
RT both nucleus and cytoplasm."
RL J. Biol. Chem. 271:22081-22089(1996).
CC -I- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
CC COMPARTMENT.
CC -I- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
CC COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CC CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
CC B (THE R2/B/PR55/B55, R3/B'/PR72/PR130/PR59 AND R5/B'/B56
CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
CC AND CELL SIGNALING MOLECULES.
CC -I- SUBCELLULAR LOCATION: Nuclear (isoforms 1 and 3).
CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS: GAMMA-1, GAMMA-2 AND GAMMA-3
CC (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: HIGHEST LEVELS IN HEART, SKELETAL MUSCLE AND
CC BRAIN. LOWER LEVELS IN PANCREAS, KIDNEY, LUNG AND PLACENTA. VERY
CC LOW LEVELS IN LIVER.
CC -I- PTM: AT LEAST ISOFORM GAMMA-3 IS PHOSPHORYLATED ON SERINE RESIDUES
CC WHILE ISOFORM GAMMA-1 IS NOT.
CC -I- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U37352; AAC50387.1; ALT_INIT.
CC EMBL; Z69030; AAC32154.1; -
CC EMBL; D26445; BAA05465.1; -
CC EMBL; L42375; AAC37603.1; -
CC Genew; HGNC:9311; PPR2R5C.
CC MIM; 601645; -
CC InterPro; IPR002554; B56.
CC Pfam; PF01603; B56; 1.
KW Nuclear protein; Phosphorylation; Alternative splicing;
KW Multigene family.
FT DOMAIN 416 422
FT VARSPLIC 443 524
FT
FT
FT VARSPLIC 443 481
FT CONFLICT 494 494
FT CONFLICT L -> R (IN REF. 3).
SQ SEQUENCE 524 AA; 61017 MW; 28EBF54550D70C19 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 524;

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|
|
|
|
Db 310 EILDV 314

RESULT 47

2A5G RABIT STANDARD; PRT; 524 AA.
AC Q28651; Q28648; Q28650; Q28652;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
DE gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit,
DE B56 gamma isoform) (PP2A, B subunit, P861 gamma isoform) (PP2A, B
DE subunit, R5 gamma isoform) (PP2A, B subunit, B' beta isoform).
GN P2P2R5C.

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

SEQUENCE FROM N.A.

RC STRAIN=New Zealand; TISSUE=Skeletal muscle;
RX MEDLINE=9616194; PubMed=9576224;
RA Geortos C., Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
RT "High complexity in the expression of the B' subunit of protein
RT phosphatase 2A0. Evidence for the existence of at least seven novel
RT isoforms."

RL J. Biol. Chem. 271:2578-2588 (1996).

CC -1- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
CC COMPARTMENT.

CC -1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
CC COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CC CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
CC B (THE R2/B/PR55/B55, R3/B'/PR72/PR130/PR59 AND R5/B'/B56
CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
CC AND CELL SIGNALING MOLECULES.

CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS, GAMMA-1/BETA-4, GAMMA-3/BETA-
CC 3 (SHOWN HERE), GAMMA-4/BETA-1 AND GAMMA-5/BETA-2; ARE PRODUCED BY
CC ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, HEART AND SPLEEN.
CC ALSO FOUND IN BRAIN AND SKELETAL MUSCLE.

CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B

CC FAMILY.

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CC -----

DR EMBL; U38191; AAC48530.1; -

DR EMBL; U37770; AAC48528.1; -

DR EMBL; U38190; AAC48529.1; -

DR EMBL; U38192; AAC48531.1; -

DR InterPro; IPR002554; B56.

DR Pfam; PF01603; B56; 1.

KW Alternative splicing: Multigene family; Nuclear protein.

FT DOMAIN 472 489 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT VARSPLIC 482 524 AOKDPKPKERPLARRKSELPODPHTKKALEAHCRADVLVPOD

FT GR -> QLVGKRKSVSTQVRKV (IN ISOFORM GAMMA-

FT 4).

FT

FT VARSPLIC 482 524 AOKDPKPKERPLARRKSELPODPHTKKALEAHCRADVLVPOD
FT GR -> VKVPG (IN ISOFORM GAMMA-5).
FT YSLCSHASTVSRKSLPMFLMETDGLPFDVQMLKTKTYSDEARQAO
FT KDPKPKERPLARRKSELPODPHTKKALEAHCRADVLVPODGR
FT -> VLKKRAI (IN ISOFORM GAMMA-1).
SQ SEQUENCE 524 AA; 60984 MW; DC4520D122DAF386 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 524;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5

|
|
|
|
Db 310 EILDV 314

RESULT 48

SYM_CHLPN

ID -SYM_CHLPN STANDARD; PRT; 551 AA.

AC Q92599; Q9JRW1;

DT 30-MAY-2000 (Rel. 39, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)

DE (MetrS).

GN METG OR CPN0122 OR CP0651.

OS Chlamydia pneumoniae (Chlamydia phila pneumoniae).

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=83558;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=CWL029;

RX MEDLINE=99206606; PubMed=10192388;

RA Kalman S., Mitchell W., Marathe R., Lammel C., Pan J., Hyman R.W.,

RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis";

RL Nat. Genet. 21:385-389 (1999).

RN [2]

RC SEQUENCE FROM N.A.

RP STRAIN=AR39;

RX MEDLINE=20150255; PubMed=10684935;

RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

RA White O., Hickey E.K., Peterson J., Utterback T., Berry K.,

RA Linher K., Weidman J., Khouri H., Craven B., Bowman C.,

RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,

RA Eisen J., Fraser C.M.;

RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia

RT pneumoniae AR39.";

RL Nucleic Acids Res. 28:1397-1406 (2000).

RN [3]

RC SEQUENCE FROM N.A.

RP STRAIN=J138;

RX MEDLINE=20330349; PubMed=10871362;

RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,

RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;

RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138

RT from Japan and CWL029 from USA.";

RL Nucleic Acids Res. 28:2311-2314 (2000).

CC -1- FUNCTION: IT IS PROBABLY ESSENTIAL FOR CELL SURVIVAL, BEING

CC REQUIRED NOT ONLY FOR ELONGATION OF PROTEIN SYNTHESIS BUT ALSO

CC FOR THE INITIATION OF ALL MENA TRANSLATION THROUGH INITIATOR

CC TRNA (FMET) AMINOACYLATION.

CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP +

CC diphosphate + L-methionyl-tRNA(Met).

CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

CC STRONG, TO CYSTEINYL-TRNA SYNTHETASE.

CC -----

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CC EMBL; AE001598; AAD18275.1; -;
 CC EMBL; AE002223; AAF38466.1; -;
 CC EMBL; AP002545; BAA98333.1; -;
 CC HSP; P00959; 1MEA.
 CC PHCI-2DPAGE; Q92959; -;
 CC TIGR; CP0651; -;
 CC InterPro; IPR002300; trna-synt 1a.
 CC InterPro; IPR001412; trna-synt 1.
 CC InterPro; IPR002304; trna-synt_met.
 CC Pfam; PF00133; trna-synt 1; 1.
 CC PRINTS; PR01041; TRNASYNTHMET.
 CC TIGRFAMs; TIGR00398; metg; 1.
 CC PROSITE; PS00178; AA TRNA LIGASE I; FALSE NEG.
 CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Metal-binding; Zinc; Complete proteome.
 FT SITE 12 22 "HIGH" REGION.
 FT SITE 330 334 "KMSKS" REGION.
 FT BINDING 333 333 ATP (BY SIMILARITY).
 FT METAL 144 144 ZINC (BY SIMILARITY).
 FT METAL 147 147 ZINC (BY SIMILARITY).
 FT METAL 157 157 ZINC (BY SIMILARITY).
 FT METAL 160 160 ZINC (BY SIMILARITY).
 FT CONFLICT 171 171 D -> G (IN REF. 1).
 FT CONFLICT 423 423 V -> A (IN REF. 1).
 SQ SEQUENCE 551 AA; 63453 MW; CAB2E38331452B19 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 551;
 Best Local Similarity 100.0%; Pred. No. 3e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 DB 529 EILDV 533

RESULT 49
 2A5D RABBIT STANDARD; PRT; 586 AA.
 AC Q28653; Q28655;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
 DE delta isoform (PP2A, B subunit, B' delta isoform) (PP2A, B subunit,
 DE B56 delta isoform) (PP2A, B subunit, PR61 delta isoform) (PP2A, B
 DE subunit, R5 delta isoform) (PP2A, B subunit, B'-gamma).
 GN PPP2R5D.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand;
 RX MEDLINE=96161994; PubMed=8576224;
 RA Csontos C., Zolnierowicz S., Bako E., Durbin S.D., Depaoli-Roach A.A.;
 RT "High complexity in the expression of the B' subunit of protein
 RT phosphatase 2A0. Evidence for the existence of at least seven novel
 RT isoforms.";
 RL J. Biol. Chem. 271:2578-2588 (1996).
 CC -1- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
 CC SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
 CC LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
 CC COMPARTMENT.
 CC -1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
 CC COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
 CC CONSTANT REGULATORY SUBUNIT (PR65 OF SUBUNIT A), THAT ASSOCIATES
 CC WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE

CC WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
 CC B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56
 CC FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
 CC AND CELL SIGNALING MOLECULES.
 CC -1- SUBCELLULAR LOCATION: Nuclear (by similarity).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
 CC FAMILY.
 CC -1- CAUTION: NOMENCLATURE USED IN REF.1 REFERS TO PP2A B SUBUNIT
 CC B' GAMMA ISOFORM, WHICH IS CITED AS PP2A B SUBUNIT DELTA-PR61
 CC ISOFORM IN LATER PUBLICATIONS.
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CC EMBL; U38193; AAC48532.1; -;
 CC EMBL; U38195; AAC48534.1; -;
 CC InterPro; IPR002554; B56.
 CC Pfam; PF01603; B56; 1.
 CC Multigene family; Nuclear protein; Repeat.
 FT DOMAIN 21 36 8 X 2 AA APPROXIMATE TANDEM REPEATS OF Q-
 FT P.
 FT DOMAIN 507 514 SH3 BINDING, CLASS I (POTENTIAL).
 FT DOMAIN 532 549 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 586 AA; 68090 MW; E149A309CDDA7495 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 586;
 Best Local Similarity 100.0%; Pred. No. 3.2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 DB 370 EILDV 374

RESULT 50
 2A5D HUMAN STANDARD; PRT; 602 AA.
 AC Q14738; Q00696; Q00494; Q15171;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit,
 DE delta isoform (PP2A, B subunit, B' delta isoform) (PP2A, B subunit,
 DE B56 delta isoform) (PP2A, B subunit, PR61 delta isoform) (PP2A, B
 DE subunit, R5 delta isoform).
 GN PPP2R5D.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA-1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=96355607; PubMed=8703017;
 RA McCright B., Rivers A.M., Audlin S., Virshup D.M.;
 RT "The B56 family of protein phosphatase 2A (PP2A) regulatory subunits
 RT encodes differentiation-induced phosphoproteins that target PP2A to
 RT both nucleus and cytoplasm.";
 RL J. Biol. Chem. 271:22081-22089 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS DELTA-1 AND DELTA-3).
 RC TISSUE=Brain cortex;
 RX MEDLINE=97324098; PubMed=9180267;
 RA Tanabe O., Gomez G.A., Nishito Y., Usui H., Takeda M.;
 RT "Molecular heterogeneity of the cDNA encoding a 74-kDa regulatory
 RT subunit (B' or delta) of human protein phosphatase 2A.";
 RL FEBS Lett. 408:52-56 (1997).

[3]
SEQUENCE FROM N.A. (ISOFORM DELTA-2), AND SEQUENCE OF 501-508;
550-559; 573-580 AND 584-601 (DELTA-1).
TISSUE=Brain cortex, and Bone marrow;
MEDLINE=96159032; PubMed=8566219;
Tanabe O., Nagase T., Murakami T., Nozaki H., Usui H., Nishito Y.,
Hayashi H., Kagamiyama H., Takeda M.,
RT "Molecular cloning of a 74-kDa regulatory subunit (B'' or delta) of
human protein phosphatase 2A.";
FEBS Lett. 379:107-111(1996).
[4]
SEQUENCE FROM N.A. (ISOFORMS DELTA-1 AND DELTA-2).
TISSUE=Colon, Eye, and Kidney;
Submitted R.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: THE B REGULATORY SUBUNIT MIGHT MODULATE SUBSTRATE
SELECTIVITY AND CATALYTIC ACTIVITY, AND ALSO MIGHT DIRECT THE
LOCALIZATION OF THE CATALYTIC ENZYME TO A PARTICULAR SUBCELLULAR
COMPARTMENT.
-1- SUBUNIT: PP2A CONSISTS OF A COMMON HETERODIMERIC CORE ENZYME,
COMPOSED OF A 36 kDa CATALYTIC SUBUNIT (SUBUNIT C) AND A 65 kDa
CONSTANT REGULATORY SUBUNIT (PR65 OR SUBUNIT A), THAT ASSOCIATES
WITH A VARIETY OF REGULATORY SUBUNITS. PROTEINS THAT ASSOCIATE
WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS
B (THE R2/B/PR55/B55, R3/B''/PR72/PR130/PR59 AND R5/B'/B56
FAMILIES), THE 48 kDa VARIABLE REGULATORY SUBUNIT, VIRAL PROTEINS,
AND CELL SIGNALING MOLECULES.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR IN INTERPHASE,
NUCLEAR DURING MITOSIS.
-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; DELTA-1 (SHOWN HERE), DELTA-2
AND DELTA-3; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- TISSUE SPECIFICITY: ISOFORM DELTA-2 IS WIDELY EXPRESSED. ISOFORM
DELTA-1 IS HIGHLY EXPRESSED IN BRAIN.
-1- INDUCTION: BY RETINOIC ACID; IN NEUROBLASTOMA CELL LINES.
-1- PTM: AT LEAST ISOFORM DELTA-1 IS PHOSPHORYLATED ON SERINE
RESIDUES.
-1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
FAMILY.

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EMBL; L76702; AB069751.1; -;
EMBL; AB000634; BAA20381.1; -;
EMBL; AB000635; BAA20382.1; -;
EMBL; D78360; BAA11372.1; -;
EMBL; BC001095; AAH01095.1; -;
EMBL; BC001175; AAH01175.1; -;
EMBL; BC010692; AAH10692.1; -;
Genew; HGNC:9312; PPF2HSD.
MIN; 601646; -;
InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
Nuclear protein; Phosphorylation; Alternative splicing; Repeat;
Multigene family.
DOMAIN 37 52 8 X 2 AA APPROXIMATE TANDEM REPEATS OF Q-
P.
DOMAIN 523 530 SH3 BINDING, CLASS I (POTENTIAL).
DOMAIN 548 565 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT VARSPPLIC 11 116 MISSING (IN ISOFORM DELTA-3).
FT VARSPPLIC 85 116 MISSING (IN ISOFORM DELTA-2).
SQ SEQUENCE 602 AA; 69991 MW; F15F71AF4E565387 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5

Db 386 EILDV 390
|||||
RESULT 51
TOPI_BACHD
ID TOPI_BACHD STANDARD; PRT; 690 AA.
AC O9KA23;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA topoisomerase I (EC 5.99.1.2) (Omega-protein) (Relaxing enzyme)
DE (Untwisting enzyme) (Swivelase).
GN TOPA OR BH2467.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maeui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
RL
CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE
CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.
CC -1- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
DNA, followed by passage and rejoining.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA
BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN
WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS
AT ONE END OF THE ENZYME-SEVERED DNA STRAND.
CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
FAMILY.

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EMBL; AP001515; BAB06186.1; -;
DR HSPP; P06612; IECL.
DR InterPro; IPR002936; DNAPrim toprim.
DR InterPro; IPR003601; DNATopi_ATP_bind.
DR InterPro; IPR003602; DNATopi_DNA_bind.
DR InterPro; IPR000380; Prok_topisomase.
DR Pfam; PF01131; Topoisom_bac; 1.
DR Pfam; PF01396; zf-C4_Topoisom; 3.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00417; PRTPI5MRASE1.
DR SMART; SM00437; TOP1AC; 1.
DR SMART; SM00436; TOP1BC; 1.
DR SMART; SM00493; TOPRIM; 1.
DR TIGRFAMs; TIGR01051; topa_bact; 1.
DR PROSITE; PS00396; TOPOISOMERASE_I_PROK; 1.
KW Isomerase; Topoisomerase; DNA-binding; Zinc-finger; Metal-binding;
Repeat; Complete proteome.
FT ZN_FING 579 605 C4-TYPE 1.
FT ZN_FING 619 647 C4-TYPE 2.
FT ZN_FING 660 683 C4-TYPE 3.
FT ACT_SITE 298 298 DNA_CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 690 AA; 78910 MW; EB3E9E0B5546256 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EILDV 5
Db 519 EILDV 523

RESULT 52
EFT2_FOWPV STANDARD; PRT; 709 AA.
ID Q9J562;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN Fowlpox virus (FPV).
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RA Alfonso C.I., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831(2000).
CC -I- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM
CC EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
CC ASSOCIATED WITH VETF.
CC -I- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
CC
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CC
CC EMBL; AF198100; AAF44515.1; -
CC Translation regulation; Activator.
CC SEQUENCE 709 AA; 82729 MW; 79C39E93A84E051C CRC64;
Query Match 100.0%; Score 23; DB 1; Length 709;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
Db 17 EILDV 21

RESULT 53
DEND RAT
ID DEND RAT STANDARD; PRT; 719 AA.
AC P50617;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Dendrin (Fragment).
GN DDN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Brain;
RC MEDLINE=97073143; PubMed=8915891;
RA Neuner-Jehle M., Denizot J.P., Borbely A.A., Mallet J.;
RT "Characterization and sleep deprivation-induced expression modulation
RT of dendrin, a novel dendritic protein in rat brain neurons.";
RL J. Neurosci. Res. 46:138-151(1996).
CC -I- MISCELLANEOUS: MODULATED BY SLEEP DEPRIVATION.
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CC
CC EMBL; X96589; CAA65407.1; -
CC Non TER
CC SEQUENCE 719 AA; 77208 MW; 89E2ED094514EAFB CRC64;
Query Match 100.0%; Score 23; DB 1; Length 719;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
Db 693 EILDV 697

RESULT 54
TLR2_BOVIN
ID TLR2_BOVIN STANDARD; PRT; 784 AA.
AC Q95L39; Q9GL66;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Toll-like receptor 2 precursor.
GN TLR2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Guinaud C.T., Dubey C., Zunker J.R., Sonstegard T.S., Jungi T.W.;
RT "Role of bovine TLR2, TLR4 and CD14 in the recognition of bacterial
RT constituents.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Cooperates with MD-2 and TLR6 to mediate the innate
CC immune response to bacterial lipoproteins and other microbial cell
CC wall components. Acts via MyD88 and IRAF6, leading to NF-kappa-B
CC activation, cytokine secretion and the inflammatory response. May
CC also promote apoptosis in response to lipoproteins (By
CC similarity).
CC -I- SUBUNIT: Binds MD-2 and TLR6 via the extracellular domain. Binds
CC MyD88 via their respective TIR domains (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -I- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -I- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).
CC
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CC
CC EMBL; AF368419; AAL16722.1; -
CC EMBL; AF310951; AAG32060.1; -
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000483; LRR_Cterm.
CC InterPro: IPR000157; TIR_domain.
CC Pfam: PF00560; LRR; 6.
CC Pfam: PF01463; LRRCT; 1.
CC Pfam: PF01582; TIR; 1.
CC PROSITE: PS50104; TIR; 1.
CC Receptor; Immune response; Inflammatory response; Signal;
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KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 784
FT DOMAIN 21 587
FT TRANSMEM 588 608
FT DOMAIN 609 784
FT REPEAT 30 51
FT REPEAT 52 74
FT REPEAT 75 98
FT REPEAT 99 122
FT REPEAT 124 147
FT REPEAT 148 172
FT REPEAT 174 196
FT REPEAT 231 254
FT REPEAT 306 330
FT REPEAT 335 358
FT REPEAT 359 384
FT REPEAT 386 411
FT REPEAT 412 436
FT REPEAT 438 456
FT REPEAT 457 476
FT REPEAT 477 499
FT REPEAT 501 521
FT REPEAT 523 546
FT DOMAIN 639 784
FT CARBOHYD 114 114
FT CARBOHYD 199 199
FT CARBOHYD 442 442
SQ SEQUENCE 784 AA; 59FDB9DFA7984C18 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 784;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 460 BILDV 464

RESULT 55
TLR2 HUMAN STANDARD; PRT; 784 AA.
AC O60603; O15454;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Toll-like receptor 2 precursor (Toll/interleukin 1 receptor-like
DE protein 4).
GN TLR2 OR TIL4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RC TISSUE=Leukocyte, and Prostate;
RX MEDLINE=98261424; PubMed=9596645;
RA Chaudhary P.M., Ferguson C., Nguyen V., Nguyen O., Massa H.F., Eby M.,
RA Jasmin A., Traak B.J., Hood L., Nelson P.S.;
RT "Cloning and characterization of two Toll/interleukin-1 receptor-like
RT genes TIL3 and TIL4: evidence for a multi-gene receptor family in
RT humans.";
RL Blood 91:4020-4027(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98118556; PubMed=9435236;
RA Rock F.L., Hardman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
RT Toll.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:5088-5093(1998).
RN [3]
RP SEQUENCE FROM N.A., AND RESPONSE TO LIPOPOLYSACCHARIDE.
RC TISSUE=Fetal lung;

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RX MEDLINE=98421677; PubMed=9751057;
RA Yang R.-B., Mark M.R., Gray A., Huang A., Xie M.H., Zhang M.,
RA Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
RT "Toll-like receptor-2 mediates lipopolysaccharide-induced cellular
RT signalling.";
RL Nature 395:284-288(1998).
RN [4]
RP RESPONSE TO BACTERIAL LIPOPROTEINS.
RX MEDLINE=99357867; PubMed=10426996;
RA Aliprantis A.O., Yang R.-B., Mark M.R., Suggett S., Devaux B.,
RA Radolf J.D., Klimpel G.R., Godowski P.J., Zychlinsky A.;
RT "Cell activation and apoptosis by bacterial lipoproteins through
RT toll-like receptor-2.";
RL Science 285:736-739(1999).
RN [5]
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF TIR DOMAIN, AND MUTAGENESIS.
RX MEDLINE=20531768; PubMed=11081518;
RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RT receptor domains.";
RL Nature 408:111-115(2000).
CC -1- FUNCTION: Cooperates with MD-2 to mediate the innate immune
CC response to bacterial lipoproteins and other microbial cell wall
CC activation. Acts via MyD88 and TRAF6, leading to NF-kappa-B
CC also promote apoptosis in response to lipoproteins. Recognizes
CC mycoplasma macrophage-activating lipopeptide-2kD (MALP-2),
CC soluble tuberculosis factor (STF), phenol-soluble modulin (PSM)
CC and B.burgdorferi outer surface protein A lipoprotein (OspA-L)
CC cooperatively with TLR6.
CC -1- SUBUNIT: Binds MD-2 and TLR6 via the extracellular domain. Binds
CC MyD88 via their respective TIR domains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Highly expressed in peripheral blood
CC leukocytes, in particular in monocytes, in bone marrow, lymph node
CC and in spleen. Also detected in lung and in fetal liver. Levels
CC are low in other tissues.
CC -1- PTM: N-glycosylated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -1- SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
CC -----
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CC -----
CC EMBL; AF051152; AAC34377.1; -.
CC EMBL; U88878; AAC34133.1; -.
CC Genew; HGNC:11848; TLR2.
CC MIM; 603028; -.
CC PDB; 1FYW; 22-NOV-00.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_Cterm.
CC InterPro; IPR003591; LRR_TYP.
CC InterPro; IPR000157; TIR_domain.
CC Pfam; PF00560; LRR; 6.
CC Pfam; PF01463; LRRCT; 1.
CC Pfam; PF01582; TIR; 1.
CC SMART; SM00082; LRRCT; 1.
CC SMART; SM00369; LRR_TYP; 2.
CC SMART; SM00255; TIR; 1.
CC PROSITE; PS0104; TIR; 1.
KW Receptor; Immune response; Inflammatory response; Signal;
KW Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein;
KW 3D-structure. 1 18 POTENTIAL.
FT SIGNAL 19 784 TOLL-LIKE RECEPTOR 2.
FT CHAIN 19 588 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 19 588
FT TRANSMEM 589 609 POTENTIAL.

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FT DOMAIN 610 784
FT REPEAT 51 74
FT REPEAT 75 98
FT REPEAT 99 122
FT REPEAT 124 147
FT REPEAT 148 172
FT REPEAT 173 196
FT REPEAT 221 244
FT REPEAT 359 384
FT REPEAT 386 411
FT REPEAT 412 436
FT REPEAT 438 456
FT REPEAT 457 476
FT REPEAT 477 499
FT REPEAT 501 521
FT DOMAIN 639 784
FT CARBOHYD 114 114
FT CARBOHYD 199 199
FT CARBOHYD 414 414
FT CARBOHYD 442 442
FT MUTAGEN 681 681
FT
FT
FT
FT
SQ SEQUENCE 726 726
SQ SEQUENCE 784 AA; 89837 MW; 7DBE6B24CF1FAF8B CRC64;

Query Match 100.0%; Score 23; DB 1; Length 784;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 460 EILDV 464

RESULT 56
TLR6 HUMAN STANDARD; PRT; 796 AA.
AC Q9Y2C9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Toll-like receptor 6 precursor.
GN TLR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=99250250; PubMed=10231569;
RA Takeuchi O., Kawai T., Sanjo H., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Takeda K., Akira S.;
RT "TLR6: A novel member of an expanding Toll-like receptor family.";
RL Gene 231:59-65(1999).
RN [2]
RP FUNCTION.
RX MEDLINE=21334385; PubMed=11441107;
RA Bulut Y., Faure E., Thomas L., Equille O., Arditi M.;
RT "Cooperation of Toll-like receptor 2 and 6 for cellular activation by
RT soluble tuberculosis factor and Borrelia burgdorferi outer surface
RT protein A lipoprotein: role of Toll-interacting protein and IL-1
RL receptor signaling molecules in Toll-like receptor 2 signaling.";
RL J. Immunol. 167:987-994(2001).
CC -I- FUNCTION: Participates in the innate immune response to Gram-
CC positive bacteria and fungi. Acts via MyD88 and TRAF6, leading to
CC NF-kappa-B activation, cytokine secretion and the inflammatory
CC response. Recognizes mycoplasma macrophage-activating
CC lipopeptide-2kD (MALP-2), soluble tuberculosis factor (STF),
CC phenol-soluble modulin (PSM) and B.burgdorferi outer surface
CC protein A lipoprotein (OspA-L) cooperatively with TLR2.
CC -I- SUBUNIT: Binds TLR2 via their respective extracellular domains.
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CC CC Binds MyD88 via their respective TIR domains (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane and
CC phagosomes (By similarity).
CC -I- TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature
CC dendritic cells, plasmacytoid pre-dendritic cells and dermal
CC microvessel endothelial cells.
CC -I- SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
CC -I- SIMILARITY: CONTAINS 1 TIR DOMAIN.
CC -I- SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
CC
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CC
CC -----
CC EMBL; AB020807; BAA78631.1; -.
CC HSP; O60603; 1FYW.
CC Genew; HGNC:16711; TLR6.
CC MIM; 605403; -.
CC InterPro; IPR001611; LRR.
CC InterPro; IPR000483; LRR_Cterm.
CC InterPro; IPR003592; LRR_Out.
CC InterPro; IPR000157; TIR_domain.
CC Pfam; PF00560; LRR; 6.
CC Pfam; PF01463; LRRCT; 1.
CC Pfam; PF01582; TIR; 1.
CC PRINTS; PR00019; LEURICHRPT.
CC SMART; SM00370; LRR; 2.
CC SMART; SM00082; LRRCT; 1.
CC SMART; SM00255; TIR; 1.
CC PROSITE; PS0104; TIR; 1.
CC Receptor; Immune response; Inflammatory response; Signal;
CC Transmembrane; Repeat; Leucine-rich repeat; Glycoprotein.
KW SIGNAL
FT CHAIN 1 31 POTENTIAL.
FT DOMAIN 32 796 TOLL-LIKE RECEPTOR 6.
FT TRANSMEM 587 607 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 608 796 CYTOPLASMIC (POTENTIAL).
FT REPEAT 51 74 LRR 1.
FT REPEAT 75 98 LRR 2.
FT REPEAT 100 120 LRR 3.
FT REPEAT 121 144 LRR 4.
FT REPEAT 158 175 LRR 5.
FT REPEAT 176 201 LRR 6.
FT REPEAT 222 248 LRR 7.
FT REPEAT 376 400 LRR 8.
FT REPEAT 402 428 LRR 9.
FT REPEAT 430 447 LRR 10.
FT REPEAT 449 472 LRR 11.
FT REPEAT 474 496 LRR 12.
FT REPEAT 498 517 LRR 13.
FT DOMAIN 640 784 TIR.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 285 285 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 359 359 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 583 583 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 796 AA; 91889 MW; 35CEAEC05BFBA8BD CRC64;

Query Match 100.0%; Score 23; DB 1; Length 796;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 406 EILDV 410
```

RESULT 57
ID ADVL HUMAN STANDARD; PRT; 819 AA:
AC 07536;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Advillin (p92).
OS Advillin (p92).
GN AVIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=98330437; PubMed=9664034;
RA Marks P.W., Arai M., Bandura J.L., Kwiatkowski D.J.;
RT "Advillin (p92): a new member of the gelsolin/villin family of actin
regulatory proteins.";
RL J. Cell Sci. 114:2129-2136(1998).
CC -!- FUNCTION: CA(2+)-REGULATED ACTIN-BINDING PROTEIN.
CC -!- TISSUE SPECIFICITY: MOST HIGHLY EXPRESSED IN THE SMALL INTESTINE
AND COLONIC LINING. WEAKER EXPRESSION ALSO DETECTED IN THE THYMUS,
PROSTATE, TESTES AND UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VILLIN/GELSOLIN FAMILY.
CC -!- SIMILARITY: CONTAINS 6 GELSOLIN-LIKE REPEATS.
CC -----
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CC -----
DR EMBL; AF041449; AAC25051.1; -
DR HSSP; P02640; 1VII.
DR InterPro; IPR001974; Gelsolin.
DR InterPro; IPR001128; VHP.
DR Pfam; PF00626; Gelsolin; 6.
DR PRINTS; PR00597; GELSOLIN.
DR SMART; SM00262; GEL; 6.
DR SMART; SM00153; VHP; 1.
KW Cytoskeleton; Calcium; Actin-binding; Capping protein; Repeat.
FT DOMAIN 1 731
FT REPEAT 731 819 HEADPIECE (BY SIMILARITY).
FT REPEAT 24 73 GELSOLIN-LIKE 1.
FT REPEAT 145 185 GELSOLIN-LIKE 2.
FT REPEAT 262 306 GELSOLIN-LIKE 3.
FT REPEAT 403 454 GELSOLIN-LIKE 4.
FT REPEAT 525 565 GELSOLIN-LIKE 5.
FT REPEAT 628 669 GELSOLIN-LIKE 6.
FT DOMAIN 784 819 VHP.
FT SITE 109 116 POLYPHOSPHOINOSITIDE BINDING (BY
FT SIMILARITY).
FT SITE 135 143 POLYPHOSPHOINOSITIDE BINDING (BY
FT SIMILARITY).
SQ SEQUENCE 819 AA; 92086 MW; 8EE1C1ED60110CB7 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 819;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||

Db 610 BILDV 614

RESULT 58

LON_TREPA
ID LON_TREPA STANDARD; PRT; 881 AA.
AC 083536;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ATP-dependent protease La (EC 3.4.21.53).
GN LON OR TP0524.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=96659876;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388(1998).
CC -!- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS IN
PRESENCE OF ATP. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED
IN THE PROTEIN SUBSTRATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Hydrolysis of large proteins such as globin,
casein and denaturated serum albumin, in presence of ATP.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16.
CC -----
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CC -----
DR EMBL; AE001227; AAC65510.1; -
DR MEROPS; S16.0PW; -
DR TIGR; TP0524; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_center.
DR InterPro; IPR001270; Chaperlin clpA/B.
DR InterPro; IPR003111; LON.
DR InterPro; IPR001984; Lon_endopep.
DR InterPro; IPR004815; Lon_fam.
DR Pfam; PF00004; AAA; 1.
DR Pfam; PF02190; LON; 1.
DR PRINTS; PR00300; CLPPROTEASEA.
DR PRINTS; PR00830; ENDOLAPTASE.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00464; LON; 1.
DR TIGRfams; TIGR00763; Lon; 1.
DR PROSITE; PS01046; LON_SER; 1.
KW Hydrolyase; Serine protease; ATP-binding; Complete proteome.
FT NP_BIND 440 447 ATP (POTENTIAL).
FT ACT_SITE 767 767 BY SIMILARITY.
SQ SEQUENCE 881 AA; 97728 MW; 7D1905CD4920B504 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 881;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||

Db 268 BILDV 272

```
RESULT 59
ID_IREL_HUMAN STANDARD; PRT; 889 AA.
AC P21339; Q14652;
DT 01-MAY-1991 (Rel. 18, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Iron-responsive element binding protein 1 (IRE-BP 1) (Iron regulatory
DE protein 1) (IRP1) (Ferritin repressor protein) (Aconitate hydratase)
DE (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase).
GN ACOL OR IREB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92150156; PubMed=1738601;
RA Hirling H., Emery-Goodman A., Thompson N., Neupert B., Seiser C.,
RA Kuehn L.;
RT "Expression of active iron regulatory factor from a full-length human
RT cDNA by in vitro transcription/translation.";
RL Nucleic Acids Res. 20:33-39(1992).
[2]
RP SEQUENCE FROM N.A.
RX TISSUE=Uterus;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE OF 53-889 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91045916; PubMed=2172968;
RA Rouault T.A., Tang C.K., Kaptain S., Burgess W.H., Haile D.J.,
RA Sananigo F., McBride O.W., Harford J.B., Klausner R.D.;
RT "Cloning of the cDNA encoding an RNA regulatory protein -- the human
RT iron-responsive element-binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7958-7962(1990).
[4]
RP SIMILARITY TO ACONITASES AND IPM ISOMERASES.
RX MEDLINE=91232935; PubMed=1903202;
RA Hentze M.W., Argos P.;
RT "Homology between IRE-BP, a regulatory RNA-binding protein,
RT aconitase, and isopropylmalate isomerase.";
RL Nucleic Acids Res. 19:1739-1740(1991).
[5]
RP ACONITASE ACTIVITY.
RX MEDLINE=92052220; PubMed=1946430;
RA Kaptain S., Downey W.E., Tang C.K., Philpott C., Haile D.J.,
RA Orloff D.G., Harford J.B., Rouault T.A., Klausner R.D.;
RT "A regulated RNA binding protein also possesses aconitase activity.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:10109-10113(1991).
CC -1- FUNCTION: BINDS TO IRON-RESPONSIVE ELEMENTS (IRES), WHICH ARE
CC STEM-LOOP STRUCTURES FOUND IN THE 5'UTR OF FERRITIN, AND DELTA
CC AMINOGLUTAMIC ACID SYNTHASE MRNAs, AND IN THE 3'UTR OF
CC TRANSFERRIN RECEPTOR MRNA. BINDING TO THE IRE ELEMENT IN FERRITIN
CC RESULTS IN THE REPRESSION OF ITS MRNA TRANSLATION. BINDING OF THE
CC PROTEIN TO THE TRANSFERRIN RECEPTOR MRNA INHIBITS THE DEGRADATION
CC OF THIS OTHERWISE RAPIDLY DEGRADED MRNA.
CC -1- FUNCTION: THIS PROTEIN ALSO EXPRESSES ACONITASE ACTIVITY.
CC -1- CATALYTIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC -----
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CC -----
CC EMBL; Z11559; CAA77651.1; -.
CC EMBL; BC018103; AAH18103.1; -.
CC EMBL; M58510; AAA69900.1; -.
CC -----
```

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DR PIR; A36203; A36203.
DR Genew; HGNC:1117; ACO1.
DR MIM; 100880; -.
DR InterPro; IPR000573; Aconitase_C.
DR InterPro; IPR001030; Aconitase_N.
DR Pfam; PF00330; aconitase; 1.
DR Pfam; PF00694; Aconitase_C; 1.
DR PRINTS; PR00415; ACONITASE.
DR PRODOM; PD000511; Aconitase_N; 1.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR KW Lyase; Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S; RNA-binding.
FT METAL 437 437 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 503 503 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 506 506 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT CONFLICT 53 71 FLVKKQDIENILHWNVQIH -> CPRTRIQNLPPWLSNKL
FT Y (IN REF. 3).
SQ SEQUENCE 889 AA; 98398 MW; E1A05AF701D46DCB CRC64;
Query Match 100.0%; Score 23; DB 1; Length 889;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 748 EILDV 752
RESULT 60
RNE_BUCAI
ID_RNE_BUCAI STANDARD; PRT; 902 AA.
AC P57429;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease E (EC 3.1.4.-) (RNase E).
GN RNE OR BU347.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: THIS PROTEIN MATURES 5S RNA FROM ITS PRECURSORS FROM
CC ALL THE RNA GENES. IT IS THE MAJOR ENDORIBONUCLEASE PARTICIPATING
CC IN RNA TURNOVER (BY SIMILARITY).
CC -1- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESSOME OR RNA
CC DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE RNE FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SI MOTIF DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP001119; BAB13052.1; -.
CC InterPro; IPR004659; RNaseEG.
CC InterPro; IPR003029; SI.
CC Pfam; PF00575; SI; 1.
CC SMART; SM00316; SI; 1.
CC TIGRFAMs; TIGR00757; RNaseEG; 1.
```


DR PROSITE; PS50126; S1; 1.
KW Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
FT DOMAIN 39 119 S1 MOTIF.
SQ SEQUENCE 902 AA; 104006 MW; C3FA00476E3C2E37 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 902;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 525 EILDV 529

RESULT 61
SYNP HUMAN STANDARD; PRT; 919 AA.
AC Q9Y6H5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Synphilin 1 (Alpha-synuclein interacting protein).
GN SNCAIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=95251592; PubMed=10319874;
RX Engelender S., Kaminsky Z., Guo X., Sharp A.H., Amaravi R.K.,
RA Kleiderlein J.J., Margolis R.L., Troncoso J.C., Lanahan A.,
RA Worley P.F., Dawson V.L., Dawson T.M., Ross C.A.;
RT "Synphilin-1 associates with alpha-synuclein and promotes the
formation of cytosolic inclusions."
RT Nat. Genet. 22:110-114 (1999).
RL Science 269:496-512 (1995).
CC -1- SUBUNIT: ASSOCIATES WITH SNCA.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN
BRAIN, HEART AND PLACENTA.
CC -1- MISCELLANEOUS: CONSTRUCTS ENCODING PORTIONS OF SNCA AND SNCAIP
CO-TRANSECTED IN MAMMALIAN CELLS PROMOTE CYTOSOLIC INCLUSIONS
RESEMBLING THE LEWY BODIES OF PARKINSON DISEASE.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC
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CC
DR EMBL; AF076929; AAD30362.1; -.
DR Genbank; HGNC:11139; SNCAIP.
DR MIN; 603779; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 2.
DR PROSITE; PS50086; ANK_REPEAT; 1.
DR POSITIVE; PS50297; ANK_REPEAT_REGION; 1.
KW Coiled coil; Repeat; ANK repeat.
FT REPEAT 349 380 ANK 1.
FT REPEAT 384 413 ANK 2.
FT REPEAT 419 448 ANK 3 (POTENTIAL).
FT REPEAT 456 485 ANK 4.
FT DOMAIN 515 552 COILED COIL (POTENTIAL).
FT REPEAT 603 632 ANK 5 (POTENTIAL).
FT REPEAT 699 729 ANK 6 (POTENTIAL).
SQ SEQUENCE 919 AA; 100380 MW; 5CE0022E0024EEA4 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 919;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 152 EILDV 156

RESULT 62
HEPA_HAEIN STANDARD; PRT; 923 AA.
ID HEPA_HAEIN
AC P44781;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RNA polymerase associated protein homolog (ATP-dependent helicase
hepa).
DE hepa).
GN HEPA OR HI0616.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McInerney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.U., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
Rd."
RT Science 269:496-512 (1995).
RL Science 269:496-512 (1995).
CC -1- SUBUNIT: BINDS TO THE RNA POLYMERASE (RNAP) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
CC
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CC
DR EMBL; U32744; AAC22275.1; -.
DR TIGR; HI0616; -.
DR InterPro; IPR001650; Helicase C.
DR InterPro; IPR000330; SNF2_N_1_
DR Pfam; PF00176; SNF2_N; 1_
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00490; HELICG; 1.
KW Helicase; ATP-binding; Complete proteome.
FT NP_BIND 175 182 ATP (BY SIMILARITY).
FT SITE 278 281 DEAH BOX.
SQ SEQUENCE 923 AA; 104405 MW; 8022403581DAADBD CRC64;

Query Match 100.0%; Score 23; DB 1; Length 923;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 70 EILDV 74

RESULT 63
GLND_RHIME STANDARD; PRT; 949 AA.
ID GLND_RHIME
AC P56884;

DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE [Protein-Pil] uridylyltransferase (EC 2.7.7.59) (PII uridylyl-
DE transferase) (Uridylyl removing enzyme) (Urase).
GN GLND OR R00396 OR SMC01124.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN
RP SEQUENCE FROM N.A.
RC MEDLINE=2117288; PubMed=11274131;
RA Rudnick P.A., Arcondeguy T., Kennedy C.K., Kahn D.;
RA "glnD and mvnIN are genes of an essential operon in Sinorhizobium
RT meliloti.";
RL J. Bacteriol. 183:2682-2685 (2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882 (2001).
CC
CC -!- FUNCTION: MODIFIES, BY URIDYLYLATION OR DEURIDYLYLATION THE PII
CC (GlnB) REGULATORY PROTEIN (BY SIMILARITY).
CC
CC -!- CATALYTIC ACTIVITY: UTP + [protein-PII] = diphosphate + uridylyl-
CC [protein-PII].
CC
CC -!- SIMILARITY: BELONGS TO THE GLND FAMILY.
CC
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CC
CC EMBL; AF227730; AAF37852.1; -;
CC EMBL; AL591783; CAC41833.1; -;
CC InterPro; IPR002912; ACT.
CC InterPro; IPR002819; HD.
CC InterPro; IPR003607; ME Pplase HDC.
CC InterPro; IPR002934; NTP_transf.
CC Pfam; PF01842; ACT; 2.
CC Pfam; PF01909; NTP_transf_2; 1.
CC Pfam; PF01966; HD; 1.
CC SMART; SM00471; HDC; 1.
KW Transferase; Nucleotidyltransferase; Nitrogen fixation;
KW Complete proteome.
SQ SEQUENCE 949 AA; 106381 MW; EF549CIB0D8540A0 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 949;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 10 EILDV 14

RESULT 64
YK15 CAEEL
ID_YK15 CAEEL STANDARD; PRT; 952 AA.
AC P46012;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Hypothetical 105.3 kDa protein C01G6.5 in chromosome III.
GN C01G6.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Berks M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 FHA DOMAIN.
CC
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CC
CC EMBL; Z35595; CAA84636.1; -;
CC WormPep; C01G6.5; CE00867.
DR InterPro; IPR000253; FHA_domain.
DR Pfam; PF00498; FHA; 1.
DR SMART; SM00240; FHA; 1.
DR PROSITE; PS50006; FHA_DOMAIN; 1.
KW Hypothetical protein.
FT DOMAIN 39 100 FHA.
SQ SEQUENCE 952 AA; 105274 MW; D9CFB0AB3C685FBE CRC64;

Query Match 100.0%; Score 23; DB 1; Length 952;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 526 EILDV 530

RESULT 65
SECA ARATH
ID_SECA ARATH STANDARD; PRT; 1021 AA.
AC Q9SV10;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Preprotein translocase secA subunit, chloroplast precursor.
GN SECA OR AT4G01800 OR T7B11.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansong W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreis M., Delsen M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzneger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Berniseiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,

RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLeay K., Mayes R.,
 RA Platt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
 RA Massenot O., Quigley F., Clabaud G., Muendlin A., Felber R.,
 RA Schnabl F., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chedof F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bieleke C.,
 RA Frishman D., Haase D., Lencke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joehu C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
 RA Chen E., Marra M., Martienssen R., McCombie W.R.,
 RA "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana";
 RT Nature 402:769-777(1999).
 CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN
 CC PROTEIN TRANSLLOCATION ACROSS THE THYLAKOID MEMBRANE IN
 CC CHLOROPLAST.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA. A MINOR FRACTION IS
 CC ASSOCIATED WITH THE THYLAKOID MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
 CC -----
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 CC -----
 DR EMBL; AC007138; AAD22642.1; -;
 DR EMBL; AL161492; CAB7750.1; -;
 DR InterPro; IPR000185; SecA.
 DR Pfam; PF01043; SecA protein; 1.
 DR PRINTS; PR00906; SECA.
 DR TIGRFAMs; TIGR00963; secA; 1.
 DR PROSITE; PS01312; SECA; 1.
 KW Protein transport; ATP-binding; Chloroplast; Translocation; Transport;
 KW Transit peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 1021 PREPROTEIN TRANSLOCASE SECA SUBUNIT.
 FT NP BIND 176 183 ATP (POTENTIAL).
 SQ SEQUENCE 1021 AA; 115114 MW; 3D2AE013DB347187 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 1021;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 BILDV 5
 Db 348 BILDV 352
 RESULT 66
 KINN MOUSE
 ID KINN_MOUSE STANDARD; PRT; 1027 AA.
 AC P33175; Q922F9;

DT 01-OCT-1993 (Rel. 27, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuronal kinesin heavy chain (NKHC) (Kinesin heavy chain isoform 5A)
 DE (Kinesin heavy chain neuron-specific 1).
 GN KIF5A OR KIF5 OR NKHC1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99000842; PubMed=9782088;
 RA Xia C., Rahman A., Yang Z., Goldstein L.S.B.;
 RT "Chromosomal localization reveals three kinesin heavy chain genes in
 RT mouse.";
 RL Genomics 52:209-213(1998).
 RN [2]
 RP SEQUENCE OF 89-231 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93077686; PubMed=1447303;
 RA Aizawa H., Sekine Y., Takemura R., Zhang Z., Nangaku M.,
 RA Hirokawa N.;
 RT "Kinesin family in murine central nervous system.";
 RL J. Cell Biol. 119:1287-1296(1992).
 CC -1- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
 CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
 CC -1- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
 CC CHAINS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CONCENTRATED IN THE CELL BODY OF THE
 CC NEURONS, PARTICULARLY IN THE PERINUCLEAR REGION.
 CC -1- DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-
 CC TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF
 CC KINESIN (IT HYDROLYZES ATP AND BINDS MICROTUBULE), A CENTRAL
 CC ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN
 CC DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
 CC INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS),
 CC VESICLES AND MEMBRANOUS ORGANELLES.
 CC -1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF067179; AAC79803.1; -;
 DR PUR; C44259; C44259.
 DR HSP; P56536; Kif5a.
 DR MGD; MGI:109564; Kif5a.
 DR InterPro; IPR001752; Kinesin_motor.
 DR Pfam; PF00225; kinesin; 1.
 DR PRINTS; PR00380; KINESINHEAVY.
 DR SMART; SM00129; KISC; 1.
 DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
 DR PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 1 330 KINESIN-MOTOR (BY SIMILARITY).
 FT DOMAIN 331 906 COILED COIL.
 FT DOMAIN 907 1027 GLOBULAR.
 FT DOMAIN 174 315 MICROTUBULE-BINDING.
 FT NP BIND 86 93 ATP (BY SIMILARITY).
 FT CONFLICT 146 146 L -> P (IN REF. 2).
 SQ SEQUENCE 1027 AA; 117089 MW; 2A48D2FD794B9194 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 1027;
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 EILDV 5
Db 179 EILDV 183

RESULT 67
KINN_HUMAN STANDARD; PRT; 1032 AA.
AC Q12840;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuronal kinesin heavy chain (NHK) (Kinesin heavy chain isoform 5A)
DE (Kinesin heavy chain neuron-specific 1).
GN KIF5A OR NHK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RX MEDLINE=94242426; PubMed=7514426;
RA Nicolas J., Navone F., Hom-Booher N., Vale R.D.;
RT "Cloning and localization of a conventional kinesin motor expressed
RT exclusively in neurons";
RL Neuron 12:1059-1072 (1994).
CC -!- FUNCTION: KINESIN IS A MICROTUBULE-ASSOCIATED FORCE-PRODUCING
CC PROTEIN THAT MAY PLAY A ROLE IN ORGANELLE TRANSPORT.
CC -!- SUBUNIT: OLIGOMER COMPOSED OF TWO HEAVY CHAINS AND TWO LIGHT
CC CHAINS.
CC -!- SUBCELLULAR LOCATION: CONCENTRATED IN THE CELL BODY OF THE
CC NEURONS, PARTICULARLY IN THE PERINUCLEAR REGION.
CC -!- TISSUE SPECIFICITY: DISTRIBUTED THROUGHOUT THE CNS BUT IS HIGHLY
CC ENRICHED IN SUBSETS OF NEURONS.
CC -!- DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR N-
CC TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF
CC KINESIN (IT HYDROLYSES ATP AND BINDS MICROTUBULE), A CENTRAL
CC ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN
CC DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
CC INTERACTS WITH OTHER PROTEINS (SUCH AS THE KINESIN LIGHT CHAINS),
CC VESICLES AND MEMBRANOUS ORGANELLES.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
CC SUBFAMILY.
CC
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CC
CC EMBL; U06698; AAA20231.1; -.
CC HSP; P56536; 2KIN.
CC Genew; HGNC:6323; KIF5A.
CC MIN; 602821;
CC InterPro; IPR001752; kinesin_motor.
CC Pfam; PF00225; kinesin; 1.
CC PRINTS; PR00380; KINESINHEAVY.
CC SMART; SM00129; KISC; 1.
CC PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
CC PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.
KW Motor protein; Microtubules; ATP-binding; Coiled coil.
FT DOMAIN 1 330 KINESIN-MOTOR (BY SIMILARITY).
FT DOMAIN 331 906 COILED COIL.
FT DOMAIN 907 1032 GLOBULAR.
FT DOMAIN 174 315 MICROTUBULE-BINDING.
FT NP_BIND 86 93 ATP (BY SIMILARITY).
SQ SEQUENCE 1032 AA; 117392 MW; 04C0C12342020794 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 1032;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EILDV 5
Db 179 EILDV 183

RESULT 68
YGFK_ECO57 STANDARD; PRT; 1032 AA.
AC Q8WD75;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein ygfK.
GN YGFK OR 24217 OR ECS3751.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Goofai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Postbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 050952;
RX MEDLINE=21156231; PubMed=11258796;
RA Havaehi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12";
RL DNA Res. 8:11-22 (2001).
RN
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CC
CC EMBL; AF005518; AAG58007.1; -.
CC EMBL; AF002563; BAB37174.1; -.
CC InterPro; IPR001450; 4Fe4S ferredoxin.
CC InterPro; IPR001327; FAD pyr redox.
CC InterPro; IPR000205; NAD_binding.
CC Pfam; PF00037; fer4; 1.
CC Pfam; PF00070; pyr redox; 1.
CC PRINTS; PR00368; FADPNR.
CC PROSITE; PS00198; 4Fe4S FERREDOXIN; 1.
KW Hypothetical protein; Iron-sulfur; 4Fe-4S; Complete proteome.
FT METAL 938 938 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 941 941 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 944 944 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 948 948 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 1032 AA; 115563 MW; C032E7D2956E738C CRC64;

Query Match 100.0%; Score 23; DB 1; Length 1032;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EILDV 5

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Db 267 EILDV 271
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RESULT 69
YGFK_ECOLI STANDARD; PRT; 1032 AA;
AC Q46811;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein ygfk.
GN YGFK OR B2878.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner P.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glaesner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474 (1997).
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CC -----
CC EMBL; U28375; AAA83059.1; -.
CC EMBL; AB000371; AAC75916.1; -.
CC EcoGene; EG13061; ygfk.
CC InterPro; IPR001450; 4Fe4S ferredoxin.
CC InterPro; IPR001327; FAD pyr redox.
CC InterPro; IPR00205; NAD-binding.
CC Pfam; PF00037; fer4; 1.
CC ProDom; PD000139; FAD pyr redox; 1.
CC PROSITE; PS00198; 4Fe4S FERREDOXIN; 1.
CC Hypothetical protein; Iiron-sulfur; 4Fe-4S; Complete proteome.
FT METAL 938 938 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 941 941 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 944 944 IRON-SULFUR (4FE-4S) (POTENTIAL).
FT METAL 948 948 IRON-SULFUR (4FE-4S) (POTENTIAL).
SQ SEQUENCE 1032 AA; 115581 MW; 588056B51BE89648 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 1032;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 267 EILDV 271

RESULT 70
SECA_SPIOL STANDARD; PRT; 1036 AA.
AC Q36795;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Preprotein translocase secA subunit, chloroplast precursor.
GN SECA.
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC OC Spermaphyta; Magnoliophyta; eudicotyledons; core eudicots;
OC OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Monatol; TISSUE=Leaf;
RX MEDLINE=95355455; PubMed=7629156;
RA Berghoefer J., Karnauchov I., Herrmann R.G., Kloessen R.B.;
RT "Isolation and characterization of a cDNA encoding the SecA protein
RT from spinach chloroplasts. Evidence for azide resistance of
RT Sec-dependent protein translocation across thylakoid membranes in
RT spinach."
RT spinach."
RL J. Biol. Chem. 270:18341-18346 (1995).
CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. LIKELY PARTICIPATES IN
CC PROTEIN TRANSLOCATION ACROSS THE THYLAKOID MEMBRANE IN
CC CHLOROPLAST.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST STROMA. A MINOR FRACTION IS
CC ASSOCIATED WITH THE THYLAKOID MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE SECA FAMILY.
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CC -----
CC EMBL; Z49124; CAA88933.1; -.
CC InterPro; IPR000185; SecA.
CC Pfam; PF01043; SECA protein; 1.
CC PRINTS; PRO0906; SECA.
CC TIGRFAMs; TIGR00963; secA; 1.
CC PROSITE; PS01312; SECA; 1.
CC Protein transport; ATP-binding; Chloroplast; Translocation; Transport;
CC Transit peptide.
FT TRANSIT 1 776 CHLOROPLAST (POTENTIAL).
FT CHAIN 777 1036 PREPROTEIN TRANSLOCASE SECA SUBUNIT.
FT NP BIND 186 193 ATP (POTENTIAL).
SQ SEQUENCE 1036 AA; 116608 MW; 23920878B49A3283 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 1036;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 357 EILDV 361

RESULT 71
DNBI_MCMVS STANDARD; PRT; 1191 AA.
AC P30672;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major DNA-binding protein (MDBP).
GN UL57 OR DBP.
OS Murine cytomegalovirus (strain Smith).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
OX NCBI_TaxID=10367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93033129; PubMed=1329325;
RA Messerle M., Keil G.M., Schneider K., Koszowski U.H.;
RT "Characterization of the murine cytomegalovirus genes encoding the
RT major DNA binding protein and the ICP18.5 homolog."
RL Virology 191:355-367 (1992).
CC -1- FUNCTION: SINGLE-STRAND DNA-BINDING PROTEIN REQUIRED FOR DNA
CC REPLICATION.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

```


RC STRAIN=K12;
RX MEDLINE=94171083; PubMed=8125343;
RA Utsami R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki S.,
RA Nakagawa H., Miwa A., Tanabe H., Noda M.;
RT "Newly identified genes involved in the signal transduction of
RT Escherichia coli K-12.";
RL Gene 140:73-77(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93173621; PubMed=1289796;
RA Utsami R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A.,
RA Taniguchi M., Noda M.;
RT "Cloning and sequence analysis of the evgAS genes involved in signal
RT transduction of Escherichia coli K-12.";
RL Nucleic Acids Symp. Ser. 27:149-150(1992).
RN [3]
RP SEQUENCE FROM N.A. (VARIANTS EVG51 AND EVG54).
RC STRAIN=K12;
RX MEDLINE=20378313; PubMed=10923791;
RA Kato A., Ohnishi H., Yamamoto K., Furuta E., Tanabe H., Utsami R.;
RT "Transcription of enrKY is regulated by the EvgA-Evgs two-component
RT system in Escherichia coli K-12.";
RL Biosci. Biotechnol. Biochem. 64:1203-1209(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Ohshima T., Oyama S., Saito N., Sato Y., Sivaundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=98194702; PubMed=9535079;
RA Petraud A.-L., Kimmel B., Weiss V., Gross R.;
RA "Specificity of the BvgAS and EvgAS phosphorelay is mediated by the
RT C-terminal Hpt domains of the sensor proteins.";
RL Mol. Microbiol. 27:875-887(1998).
CC -1- FUNCTION: Member of the two-component regulatory system evgs/evga.
CC Phosphorylates evga via a four-step phosphorelay in response to
CC environmental signals.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- PTM: Activation requires a sequential transfer of a phosphate
CC group from a His in the primary transmitter domain, to a Asp in
CC the receiver domain and to a His in the secondary transmitter
CC domain.
CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.

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CC -----
CC ENBL; D14008; BAA03108.1; -
DR ENBL; AF201840; AAF17563.1; -
DR ENBL; AF201841; AAF17564.1; -
DR ENBL; AE000325; AAC75429.1; -
DR ENBL; D90867; BAA16241.1; -
DR PIR; JU0221; JU0221.
DR HSSP; P06143; IUDR.
DR EcoGene; EG11610; evgs.
DR InterPro; IPR003594; AtPbind ATPase.
DR InterPro; IPR004359; HIS_KIN_sig.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR002570; Hpt.
DR InterPro; IPR001789; Response_reg.
DR InterPro; IPR001311; SBP/glu_receptor.
DR InterPro; IPR001638; SBP_bac_3.
DR Pfam; PF00072; response_reg_1.
DR Pfam; PF00497; SBP_bac_3; 1.
DR Pfam; PF00512; signal; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00073; HPT; 1; 1.
DR SMART; SM00388; H18KA; 1.
DR SMART; SM00062; PBpb; 2.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS01019; HIS_KIN; 1.
DR PROSITE; PS01110; RESPONSE REGULATORY; 1.
DR Sensory transduction; Transferrase; Kinase; Phosphorylation;
KW Transmembrane; Inner membrane; Signal; Complete proteome.
FT SIGNAL 1 21
FT CHAIN 22 1197
FT DOMAIN 22 325
FT TRANSMEM 326 345
FT DOMAIN 347 537
FT TRANSMEM 538 558
FT DOMAIN 559 1197
FT DOMAIN 718 938
FT DOMAIN 960 1074
FT DOMAIN 1075 1197
FT MOD_RES 721 721
FT MOD_RES 1009 1009
FT MOD_RES 1137 1137
FT VARIANT 577 577
FT VARIANT 701 701
FT CONFLICT 152 152
FT CONFLICT 242 243
FT CONFLICT 275 275
FT CONFLICT 420 421
FT CONFLICT 739 739
FT CONFLICT 758 758
FT CONFLICT 761 761
FT CONFLICT 877 877
FT CONFLICT 1045 1045
FT CONFLICT 1074 1074
SQ SEQUENCE 1197 AA; 134742 MW; E8E1DE0F797B1278 CRC64;
Query Match 100.0%; Score 23; DB 1; Length 1197;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 767 EILDV 771
RESULT 74
RPOD SYNY3
ID _RPOD SYNY3 STANDARD; PRT; 1317 AA.
AC P73334;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase delta chain (EC 2.7.7.6).
RPOC2 OR SLL1789.
OS *Synechocystis* sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=11148;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,
RA Yanada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -1- SUBUNIT: IN CYANOBACTERIA THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, GAMMA, AND DELTA.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90905; BAA17364.1; -;
DR HSSP; Q9KWU6; 1HQM.
DR InterPro; IPR000722; RNA_pol_A.
DR InterPro; IPR002879; RNA_pol_A2.
DR Pfam; PF00623; RNA_pol_A; 1.
DR Pfam; PF01854; RNA_pol_A2; 2.
KW Transferase; DNA-directed RNA polymerase; Transcription;
KW Complete proteome.
SQ SEQUENCE 1317 AA; 144776 MW; 27B6970469E7B551 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1063 EILDV 1067

RESULT 75
ID_DP2L_HALN1 STANDARD; PRT; 1370 AA.
AC Q9HWX8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: Hsp-
DE NRC1 polC intein (Hsp-NRC1 pol2 intein)].
DE POLC OR POLA2 OR VNC2338G.
GN *Halobacterium* sp. (strain NRC-1).
OS Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Rosenbarger T.A., Beck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omar A.D.,
RT Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of *Halobacterium* species NRC-1";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- FUNCTION: POSSESSES TWO ACTIVITIES: A DNA SYNTHESIS (POLYMERASE)
CC AND AN EXONUCLEOLYTIC ACTIVITY THAT DEGRADES SINGLE STRANDED DNA
CC IN THE 3' TO 5' DIRECTION. HAS A TEMPLATE-PRIMER PREFERENCE WHICH
CC IS CHARACTERISTIC OF A REPLICATIVE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- CATALYTIC ACTIVITY: Degradation of single-stranded DNA. It acts
CC progressively in a 3'-to 5'-direction, releasing nucleoside 5'-
CC phosphates.
CC -1- SUBUNIT: HETERODIMER OF A LARGE SUBUNIT AND A SMALL SUBUNIT (BY
CC SIMILARITY).
CC -1- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES
CC A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
CC FOLLOWED BY PEPTIDE LIGATION (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARCHAEAL DNA POLYMERASE II FAMILY.
CC
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CC -----
DR EMBL; AE005116; AAC20443.1; -;
DR InterPro; IPR003586; Hedgehog_hintC.
DR InterPro; IPR003587; Hedgehog_hintN.
DR InterPro; IPR002203; Intein.
DR InterPro; IPR004475; PolC_DP2.
DR SMART; SM00305; HintC; 1.
DR SMART; SM00306; HintN; 1.
DR TIGRfams; TIGR00354; polC; 1.
DR PROSITE; PS50818; INTEIN_N_TER; 1.
DR PROSITE; PS50817; INTEIN_C_TER; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW Nuclease; Exonuclease; DNA-binding; Multifunctional enzyme;
KW Autocatalytic cleavage; Protein splicing; Complete proteome.
FT CHAIN 1 925 DNA POLYMERASE II LARGE SUBUNIT, 1ST PART
FT (POTENTIAL).
FT CHAIN 926 1120 HSP-NRC1 POLC INTEIN (POTENTIAL).
FT CHAIN 1121 1370 DNA POLYMERASE II LARGE SUBUNIT, 2ND PART
FT (POTENTIAL).
SQ SEQUENCE 1370 AA; 150295 MW; 07878AA9976790C9 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 1370;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 424 EILDV 428

Search completed: February 8, 2003, 10:24:03
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:22:23 ; Search time 28 Seconds
(without alignments)
36.794 Million cell updates/sec

Title: US-09-251-073A-16

Perfect score: 23

Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%
Listing first 100 summaries

Database :

SPRMBL_21: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	14	10	P82341
2	23	100.0	50	16	Q927L9
3	23	100.0	70	3	Q9C2B4
4	23	100.0	90	16	Q8XII2
5	23	100.0	91	2	Q8VMP3
6	23	100.0	100	11	Q9D4R8
7	23	100.0	116	11	Q9JKS1
8	23	100.0	117	11	Q9JKS2
9	23	100.0	117	11	Q9JKS0
10	23	100.0	117	11	Q9JKR8
11	23	100.0	119	17	O28742
12	23	100.0	119	17	Q9HQG9
13	23	100.0	139	17	Q8U222
14	23	100.0	146	16	Q8X335
15	23	100.0	147	16	Q8Z5E6
16	23	100.0	147	16	O53866

17	23	100.0	159	11	Q8RIU7	Q8RIU7 mus musculus
18	23	100.0	163	5	Q8SVG3	Q8SVG3 encephalito
19	23	100.0	164	17	Q8TZ22	Q8TZ22 methanopyru
20	23	100.0	169	16	Q8ZR70	Q8ZR70 salmonella
21	23	100.0	169	16	Q8Z8P8	Q8Z8P8 salmonella
22	23	100.0	171	3	Q9US90	Q9US90 schizosacch
23	23	100.0	172	5	Q9NIV2	Q9NIV2 drosophila
24	23	100.0	174	16	Q97IB1	Q97IB1 clostridium
25	23	100.0	174	16	Q8ZC15	Q8ZC15 versinia pe
26	23	100.0	175	17	Q8TV45	Q8TV45 methanopyru
27	23	100.0	176	2	Q9P213	Q9P213 streptococ
28	23	100.0	180	2	Q9Z3N7	Q9Z3N7 rhizobium s
29	23	100.0	180	16	Q97QD9	Q97QD9 streptococ
30	23	100.0	183	17	Q8TVE1	Q8TVE1 methanopyru
31	23	100.0	186	6	Q9WZ31	Q9WZ31 bos taurus
32	23	100.0	194	17	Q8ZU30	Q8ZU30 pyrobaculum
33	23	100.0	200	10	Q9STJ1	Q9STJ1 arabidopsis
34	23	100.0	208	3	O13501	O13501 phanerochae
35	23	100.0	212	4	Q9S609	Q9S609 homo sapien
36	23	100.0	219	2	Q53253	Q53253 rhizobium t
37	23	100.0	222	16	Q9WY98	Q9WY98 thermotoga
38	23	100.0	226	2	Q9L6U6	Q9L6U6 pseudomonas
39	23	100.0	231	16	Q8UA80	Q8UA80 agrobacteri
40	23	100.0	242	17	O27260	O27260 methanobact
41	23	100.0	246	2	Q9FDJ6	Q9FDJ6 lactobacill
42	23	100.0	250	16	Q8XE09	Q8XE09 escherichia
43	23	100.0	253	16	O51655	O51655 borrelia bu
44	23	100.0	256	5	O44520	O44520 caenorhabdi
45	23	100.0	266	16	Q92223	Q92223 rhizobium m
46	23	100.0	267	17	Q97WL9	Q97WL9 sulfolobus
47	23	100.0	268	10	Q94BW7	Q94BW7 cicor ariet
48	23	100.0	270	2	O24845	O24845 acinetobact
49	23	100.0	271	4	Q9H027	Q9H027 homo sapien
50	23	100.0	274	11	Q9EQ23	Q9EQ23 rattus norv
51	23	100.0	277	11	Q921S2	Q921S2 mus musculu
52	23	100.0	282	2	Q52412	Q52412 thermophili
53	23	100.0	285	17	Q8TJN0	Q8TJN0 methanosaer
54	23	100.0	287	16	Q9CN70	Q9CN70 pasteurella
55	23	100.0	290	5	O17829	O17829 caenorhabdi
56	23	100.0	304	2	Q8RLZ4	Q8RLZ4 haemophilus
57	23	100.0	307	16	Q9JUD6	Q9JUD6 neisseria m
58	23	100.0	307	16	Q9JS34	Q9JS34 neisseria m
59	23	100.0	308	2	Q9X9K3	Q9X9K3 vibrio para
60	23	100.0	312	3	O74864	O74864 schizosacch
61	23	100.0	314	11	Q8R342	Q8R342 mus musculu
62	23	100.0	317	6	Q9GMV1	Q9GMV1 macaca fasc
63	23	100.0	321	16	Q97PP0	Q97PP0 streptococ
64	23	100.0	321	16	Q9W556	Q9W556 streptococ
65	23	100.0	322	16	Q9RJ06	Q9RJ06 streptomyce
66	23	100.0	324	4	Q96F52	Q96F52 homo sapien
67	23	100.0	324	16	O25779	O25779 helicobacte
68	23	100.0	324	16	Q9ZK51	Q9ZK51 helicobacte
69	23	100.0	329	17	Q9E580	Q9E580 archaeoglob
70	23	100.0	333	16	Q9PR68	Q9PR68 ureaplasma
71	23	100.0	337	16	Q8YU24	Q8YU24 anabaena ep
72	23	100.0	338	17	Q97CD7	Q97CD7 streptomyce
73	23	100.0	339	2	Q93HG3	Q93HG3 streptomyce
74	23	100.0	344	2	O57369	O57369 borrelia bu
75	23	100.0	344	12	Q8VJG8	Q8VJG8 swinepox vi
76	23	100.0	351	3	O42781	O42781 pneumocysti
77	23	100.0	351	6	O02816	O02816 cryptococcus
78	23	100.0	357	3	O74876	O74876 schizosacch
79	23	100.0	359	10	Q9FLR9	Q9FLR9 arabidopsis
80	23	100.0	366	16	Q8Z9U8	Q8Z9U8 versinia pe
81	23	100.0	366	16	Q8Z2N5	Q8Z2N5 salmonella
82	23	100.0	366	17	Q97IY1	Q97IY1 sulfolobus
83	23	100.0	367	16	Q8UIP4	Q8UIP4 agrobacteri
84	23	100.0	368	10	Q9LSR0	Q9LSR0 arabidopsis
85	23	100.0	375	10	Q9SMF0	Q9SMF0 hordeum vul
86	23	100.0	379	4	O95617	O95617 homo sapien
87	23	100.0	384	4	Q96B13	Q96B13 homo sapien
88	23	100.0	385	5	P91106	P91106 caenorhabdi
89	23	100.0	386	16	Q9WZY0	Q9WZY0 thermotoga

90 23 100.0 388 17 Q8ULR6
 91 23 100.0 394 11 Q99WD1
 92 23 100.0 394 11 Q9R0E0
 93 23 100.0 394 11 Q88693
 94 23 100.0 402 2 Q937Y3
 95 23 100.0 400 16 Q66448
 96 23 100.0 403 10 Q9S237
 97 23 100.0 403 17 Q8TWG7
 98 23 100.0 407 17 Q73996
 99 23 100.0 408 11 Q9D3Y6
 100 23 100.0 408 16 Q55864

ALIGNMENTS

RESULT 1
 P82341
 ID P82341 PRELIMINARY; PRT; 14 AA.
 AC P82341;
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Unknown protein from 2D-page of thylakoid (SPOT251) (Fragment).
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 OX NCBI_TaxID=3888;
 RN [1]
 RP SEQUENCE, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RC STRAIN=CV, DE GRACE, TISSUE=LEAF;
 RX MEDLINE=20181728; PubMed=10715320;
 RA Peltier J.-B., Friso G., Kalume D.E., Roepstorff P., Nilsson F.,
 RA Adamska I., van Wijk K.J.;
 RT "Proteomics of the chloroplast: systematic identification and
 RT targeting analysis of luminal and peripheral thylakoid proteins.";
 RL Plant Cell 12:319-341(2000).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN OR
 CC PERIPHERY.
 CC -1- DEVELOPMENTAL STAGE: UNFOLDED AND FULLY DEVELOPED LEAVES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.5. ITS MW IS: 16.9 KDA.
 KW Chloroplast; Thylakoid membrane.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1590 MW; 6D968D2994D0185B CRC64;

Query Match 100.0%; Score 23; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 7 EILDV 11

RESULT 2
 Q9Z7L9
 ID Q9Z7L9 PRELIMINARY; PRT; 50 AA.
 AC Q9Z7L9;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein CPN0685.
 GN CPN0685 OR CPJ0685.
 OS Chlamydia pneumoniae (Chlamydia pneumoniae).
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiales.
 OX NCBI_TaxID=83558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206606; PubMed=10192388;
 RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,

RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-389(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20330349; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
 RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000).
 DR ENBL; AE001651; AAD18824.1; -;
 DR ENBL; AP002547; BRA98892.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 50 AA; 5959 MW; 4A8961A037A16495 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 50;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 7 EILDV 11

RESULT 3
 Q9C2D4
 ID Q9C2D4 PRELIMINARY; PRT; 70 AA.
 AC Q9C2D4;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 7.8 kDa protein.
 GN 9G6.310.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; AL513463; CAC28779.2; -;
 DR InterPro; IPR001901; SecE.
 DR InterPro; IPR004795; SecE_euk_arch.
 DR Pfam; PF00584; SecE; 1.
 DR ProDom; PD010355; SecE_euk_arch; 1.
 DR TIGRFAMs; TIGR00327; secE_euk_arch; 1.
 DR PROSITE; PS01067; SECE_SEQ61G; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 70 AA; 7809 MW; ED4EC64FE6B2E9BC CRC64;

Query Match 100.0%; Score 23; DB 3; Length 70;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 7 EILDV 11

RESULT 4
 Q8XII2
 ID Q8XII2 PRELIMINARY; PRT; 90 AA.
 AC Q8XII2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	Probable cell division topological specificity factor.
MNE	MNE OR CPE2137.
GN	Clostridium perfringens.
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC	Clostridiales; Clostridiaceae; Clostridium.
OX	NCBI_TaxID=1502;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=13 / TYPE A;
RX	PubMed=11792842;
RA	Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA	Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT	"Complete genome sequence of Clostridium perfringens, an anaerobic
RT	flesh-eater.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR	EWBL; AP003193; BAB81843.1; -;
KW	Cell division; Complete proteome.
SQ	SEQUENCE 90 AA; 10128 MW; F88B16F9580ACD CRC64;
	Query Match 100.0%; Score 23; DB 16; Length 90;
	Best Local Similarity 100.0%; Pred. No. 4.1e+02;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 EILDV 5
Dd	
	43 EILDV 47
RESULT 5	
ID	Q8VMP3 PRELIMINARY; PRT; 91 AA.
AC	Q8VMP3;
DT	01-MAR-2002 (TrEMBLrel. 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	Hypothetical protein 10.3 kDa protein.
OS	Pseudomonas putida.
OG	Plasmid pMW0.
OC	Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC	Pseudomonas.
OX	NCBI_TaxID=303;
RN	[1]
RP	SEQUENCE FROM N.A.
RT	Greated A., Lamberton L., Williams P.A., Thomas C.M.;
RT	"Complete nucleotide sequence of IncP-9 plasmid pMW0.";
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EWBL; AJ344068; CAC86746.1; -;
KW	Hypothetical protein; Plasmid.
SQ	SEQUENCE 91 AA; 10325 MW; 314F73E8672166CA CRC64;
	Query Match 100.0%; Score 23; DB 2; Length 91;
	Best Local Similarity 100.0%; Pred. No. 4.1e+02;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 EILDV 5
Dd	
	16 EILDV 20
RESULT 6	
ID	Q9D4R8 PRELIMINARY; PRT; 100 AA.
AC	Q9D4R8;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE	4930568L2IRIK protein.
GN	4930568L2IRIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI TaxID=10090;

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ID Q9JKS2 PRELIMINARY; PRT; 117 AA.
AC Q9JKS2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE C-kit receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BROWN NORWAY; TISSUE=TESTIS, AND BRAIN;
RA Gangadharan S., Ali S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT male rat testis.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228307; AAF69130.1; -.
DR InterPro; IPR003600; IG_like.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12635 MW; E2141AF47115EE78 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 76 EILDV 80

RESULT 9
ID Q9JKS0 PRELIMINARY; PRT; 117 AA.
AC Q9JKS0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE C-kit receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BROWN NORWAY; TISSUE=TESTIS;
RA Gangadharan S., Ali S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT male rat testis.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228309; AAF69132.1; -.
DR InterPro; IPR003600; IG_like.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12611 MW; E7BEC87B579CB678 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 76 EILDV 80

RESULT 10
ID Q9JKR8 PRELIMINARY; PRT; 117 AA.

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AC Q9JKR8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE C-kit receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BROWN NORWAY; TISSUE=TESTIS;
RA Gangadharan S., Ali S.;
RT "RT-PCR generated mRNA transcript from proven infertile Brown Norway
RT male rat testis.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF228311; AAF69134.1; -.
DR InterPro; IPR003600; IG_like.
DR SMART; SM00410; IG_like; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12641 MW; F3F8DC3F1288F378 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 76 EILDV 80

RESULT 11
ID Q28742 PRELIMINARY; PRT; 119 AA.
AC Q28742;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein AF1530.
GN AF1530.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000997; AAB89718.1; -.
DR TIGR; AF1530; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 119 AA; 14025 MW; 7F75DA93B80C15C CRC64;

Query Match 100.0%; Score 23; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 BILDV 5
Db 109 BILDV 113

RESULT 12
Q9HQG9 PRELIMINARY; PRT; 119 AA.
AC Q9HQG9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng1169C.
GN Vng1169C.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Laaky S.R., Baliga N.S., Thorason V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlshochder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005045; AAG19546.1; -.
KW Complete proteome.
SQ SEQUENCE 119 AA; 13648 MW; 585905ABA983B9B1 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 110 BILDV 114

RESULT 13
Q8U2Z2 PRELIMINARY; PRT; 139 AA.
AC Q8U2Z2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PF0686.
GN PF0686.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VCI / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE010189; AAL80810.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 139 AA; 16222 MW; 0879C8B7133FCE1A CRC64;

Query Match 100.0%; Score 23; DB 17; Length 139;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 111 BILDV 114

RESULT 14
Q8X935 PRELIMINARY; PRT; 146 AA.
AC Q8X935;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative PTS enzyme II B component.
GN YADI OR Z0140 OR ECS0133.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouais K.,
RA Apodaca J., Anantharaman I.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005189; AAG54433.1; -.
DR EMBL; AP002550; BAB33556.1; -.
DR InterPro; IPR004701; EIIA-man.
DR Pfam; PF03610; EIIA-man; 1.
KW Complete proteome.
SQ SEQUENCE 146 AA; 16568 MW; 8E2BB95CF7BC1CED CRC64;

Query Match 100.0%; Score 23; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 15 BILDV 19

RESULT 15
Q8Z5E6 PRELIMINARY; PRT; 147 AA.
AC Q8Z5E6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative exported protein.
GN STY2351.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
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RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
DR EMBL; AL627273; CAD02501.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 147 AA; 16938 MW; 70B44C913F9CC8A4 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
   |||||
Db 98 EILDV 102

RESULT 16
O53866 PRELIMINARY; PRT; 147 AA.
AC O53866
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein Rv0854.
GN Rv0854 OR MT0043.47 OR MT0877.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV.
RX MEDLINE=98295987; PubMed=9634230;
RA Gordon S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Cole S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Davlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / OSHKOSH;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022004; CAAL1760.1; -.
DR EMBL; AE006976; AAK45118.1; -.
DR TIGR; MT0877; -.
DR TuberculList; Rv0854; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 147 AA; 16345 MW; D9B55F6B86293E07 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 EILDV 5
   |||||
Db 17 EILDV 21

RESULT 17
Q8RIU7 PRELIMINARY; PRT; 159 AA.
AC Q8RIU7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 18.9 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC023062; AAB23062.1; -.
KW Hypothetical protein.
SQ SEQUENCE 159 AA; 18896 MW; 349F26D187132A15 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 159;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
   |||||
Db 8 EILDV 12

RESULT 18
Q8SVG3 PRELIMINARY; PRT; 163 AA.
AC Q8SVG3
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein ECU05_1480.
GN ECU05_1480.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1.
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi."
RL Nature 414:450-453(2001).
DR EMBL; AL590445; CAD28668.1; -.
KW Hypothetical protein.
SQ SEQUENCE 163 AA; 18931 MW; 3A36178CB48421FF CRC64;

Query Match 100.0%; Score 23; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
   |||||

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Db 27 EILDV 31
Query Match 100.0%; Score 23; DB 16; Length 169;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 19
Q8TZ22 PRELIMINARY; PRT; 164 AA.
AC Q8TZ22;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorisomate--pyruvate lyase family enzyme.
GN UBIC OR MK0119.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozayavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
KW EMBL; AEO10311; AAM01336.1; -.
KW Lyase; Pyruvate; Complete proteome.
SQ SEQUENCE 164 AA; 19130 MW; 02861FCD99CB69D CRC64;

Query Match 100.0%; Score 23; DB 17; Length 164;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 125 EILDV 129

RESULT 20
Q8ZR70 PRELIMINARY; PRT; 169 AA.
AC Q8ZR70;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphoribosylaminoimidazole carboxylase = AIR carboxylase, catalytic
DE subunit (EC 4.1.1.21).
GN PURS OR STM0534.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du P., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856 (2001).
RX EMBL; AE008720; AAL19488.1; -.
DR InterPro; IPR000031; AIR_carboxyl.
DR Pfam; PF00731; AIRC; 1.
DR TIGRFAMs; TIGR01162; purE; 1.
KW Lyase; Complete proteome.
SQ SEQUENCE 169 AA; 17794 MW; 8F16C7B27311B9B8 CRC64;
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Qy 1 EILDV 5
|||||
Db 31 EILDV 35

RESULT 21
Q8Z8P8 PRELIMINARY; PRT; 169 AA.
AC Q8Z8P8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phosphoribosylaminoimidazole carboxylase catalytic subunit.
GN STY0582.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feitwell T., Hamlin N., Haque A., Hien T.F., Holroyd S., Jørgensen K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852 (2001).
DR EMBL; AL627267; CAD05018.1; -.
DR InterPro; IPR000031; AIR_carboxyl.
DR Pfam; PF00731; AIRC; 1.
DR TIGRFAMs; TIGR01162; purE; 1.
KW Complete proteome.
SQ SEQUENCE 169 AA; 17753 MW; AF55C3E11623BCEA CRC64;

Query Match 100.0%; Score 23; DB 16; Length 169;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 31 EILDV 35

RESULT 22
Q9US90 PRELIMINARY; PRT; 171 AA.
AC Q9US90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical nuclear protein (Fragment).
GN SPCC330.04C.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=968 H90;
RX MEDLINE=20223868; PubMed=10759889;
RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hiraoka Y.;
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RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library."
RL Genes Cells 5:169-190(2000).
DR EMBL; AB027955; BAA87259.1; -.
KW Nuclear protein.
FT NON_TER 1 1
FT NON_TER 171 171
SQ SEQUENCE 171 AA; 21395 MW; 30012B18345508BE CRC64;

Query Match 100.0%; Score 23; DB 3; Length 171;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 151 EILDV 155

RESULT 23
Q9NIV2 PRELIMINARY; PRT; 172 AA.
ID Q9NIV2
AC Q9NIV2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Stellate protein.
GN STL2DOR.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Shevel'yov Y.Y., Kalmykova A.I.;
RT "Stellate orthon provides a poly(A) signal for bendless mRNA."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF192309; AA835172.1; -.
DR FlyBase; FBgn003523; Ste.
DR FlyBase; FBgn0044817; STL2DOR.
DR InterPro; IPR000704; CAS_Kinase_II.
DR Pfam; PF01214; CK II beta; 1.
DR PRINTS; PR00472; CAS_KINASEII.
DR PROSITE; PS01101; CK2_BETA; 1.
SQ SEQUENCE 172 AA; 19525 MW; A2C8752F3A976F8B CRC64;

Query Match 100.0%; Score 23; DB 5; Length 172;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 46 EILDV 50

RESULT 24
Q97IB1 PRELIMINARY; PRT; 174 AA.
ID Q97IB1
AC Q97IB1;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Uncharacterized conserved protein (coiled-coil).
GN CAC1739.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007683; AAK79705.1; -.
KW Complete proteome.
SQ SEQUENCE 174 AA; 20244 MW; 80EA9CA386E436BF CRC64;

Query Match 100.0%; Score 23; DB 16; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 32 EILDV 36

RESULT 25
Q8ZC15 PRELIMINARY; PRT; 174 AA.
ID Q8ZC15
AC Q8ZC15;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Shikimate kinase II (EC 2.7.1.71).
GN AROL OR YPO3215.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Farraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
DR EMBL; AJ414156; CAC92450.1; -.
DR InterPro; IPR000623; Shik_kinase.
DR Pfam; PF01202; SKI; 1.
DR PRINTS; PR01100; SHIKIMTKINASE.
DR PROSITE; PS01128; SHIKIMATE_KINASE; UNKNOWN_1.
KW Kinase; Transferase; Complete proteome.
SQ SEQUENCE 174 AA; 18864 MW; 8D9A1E8BF88730D6 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 174;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 131 EILDV 135

RESULT 26
Q8TV45 PRELIMINARY; PRT; 175 AA.
ID Q8TV45
AC Q8TV45;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Uncharacterized protein.
GN MK1555.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;


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OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva V.V., Makarova K.S., Polushin N.N.,
RA Scherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Nataly D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649 (2002).
DR EMBL; AE010445; AA020768.1; -.
KW Complete proteome.
SQ SEQUENCE 175 AA; 19325 MW; 695D9BAFFDIAC73B CRC64;

Query Match 100.0%; Score 23; DB 17; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 144 EILDV 148

RESULT 27
Q9F213 PRELIMINARY; PRT; 176 AA.
AC Q9F213
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Y1bN-like hypothetical protein.
GN Y1bN-LIKE
OS Streptococcus gordonii Challis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=29390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHALLIS;
RA Minick P., Vickerman M.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12643; AA332547.1; -.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 19929 MW; B73E430114725CFP CRC64;

Query Match 100.0%; Score 23; DB 2; Length 176;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 32 EILDV 36

RESULT 28
Q9Z3N7 PRELIMINARY; PRT; 180 AA.
AC Q9Z3N7
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Modulation protein B (Fragment).
OS Rhizobium sp. WSM870.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=87226;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WSM870;
RX MEDLINE=99261640; PubMed=10331255;
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RA Wernegreen J.J., Riley M.A.;
RT "Comparison of the evolutionary dynamics of symbiotic and housekeeping
RT loci: a case for the genetic coherence of rhizobial lineages.";
RL Mol. Biol. Evol. 16:98-113 (1999).
DR EMBL; AF063458; AAD14328.1; -.
DR InterPro; IPR002509; Polysac_deacet.
DR Pfam; PF01522; Polysac_deacet; 1.
FT NON_TER 1
SQ SEQUENCE 180 AA; 19338 MW; 898CCF39389C655A CRC64;

Query Match 100.0%; Score 23; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 29
Q97QD9 PRELIMINARY; PRT; 180 AA.
AC Q97QD9
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein Sp1280.
GN Sp1280.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapfel E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae";
RL Science 293:498-506 (2001).
DR EMBL; AE007427; AAK75384.1; -.
DR TIGR; Sp1280; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 180 AA; 20399 MW; 3898616FB9EEF6E2 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 33 EILDV 37

RESULT 30
Q8TVE1 PRELIMINARY; PRT; 183 AA.
AC Q8TVE1
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA-directed RNA polymerase subunit E'.
GN RPOE1 OR MK1451.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyraceae;
OC Methanopyrus.
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OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RA MEDLINE=21927647; PubMed=11930014;
RX Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natile D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozlovskiy S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010437; AAM02664.1; -
KW DNA-directed RNA polymerase; Complete proteome.
SQ SEQUENCE 183 AA; 20754 MW; C43AA6784B63750D CRC64;

Query Match 100.0%; Score 23; DB 17; Length 183;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 56 EILDV 60

RESULT 31
Q9MZ31 PRELIMINARY; PRT; 186 AA.
ID Q9MZ31
AC Q9MZ31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibronectin variable region (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA De Candia L.M., Rodgers R.J.;
RA "Characterization of the expression of the alternative splicing of ED-
RT A, ED-B and V regions of fibronectin mRNA in bovine ovarian follicles
RT and corpora lutea.";
RL Reprod. Fertil. Dev. 0:0-0(2000).
DR EMBL; AF260305; AAF91381.1; -
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
FT NON_TER 1
FT NON_TER 186
SQ SEQUENCE 186 AA; 20378 MW; 39558D7AA23A9A29 CRC64;

Query Match 100.0%; Score 23; DB 6; Length 186;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 22 EILDV 26

RESULT 32
Q8ZU30 PRELIMINARY; PRT; 194 AA.
ID Q8ZU30
AC Q8ZU30;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE2972.
GN PAE2972.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;

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OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009904; AAL64578.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 194 AA; 21893 MW; 558DA7CC8AA4BF31 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 194;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 123 EILDV 127

RESULT 33
Q9STJ1 PRELIMINARY; PRT; 200 AA.
ID Q9STJ1
AC Q9STJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 22.8 kDa protein.
GN T4C9.40 OR A74G12200.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Peters S.A., van Staveren M., Dirkee W., Stiekema W.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Mannhaupt G.,
RA Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Peters S.A., van Staveren M., Dirkee W., Stiekema W., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL080318; CAB45967.1; -
DR EMBL; AL161533; CAB78263.1; -
DR InterPro; IPR001878; Znf.CCHC.
DR Pfam; PF00098; zf-CCHC; 1.
DR SMART; SM00343; Znf.C2HC; 1.
KW Hypothetical protein.
SQ SEQUENCE 200 AA; 22842 MW; 637CDFD14AEA7B16 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 66 EILDV 70

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RESULT 34
O13501
ID O13501 PRELIMINARY; PRT; 208 AA.
AC O13501; 1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (Fragment).
GN CYP63-1A.
OS Phanerochaete chrysosporium.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Corticiaceae; Phanerochaete.
OX NCBI_TaxID=5306;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BU-1;
RX MEDLINE=97355939; PubMed=9212420;
RA Kullman S.W., Matsumura F.;
RT "Identification of a novel cytochrome P-450 gene from the white rot
fungus Phanerochaete chrysosporium.";
RL Appl. Environ. Microbiol. 63:2741-2746(1997).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AF005475; AAB63277.1; -.
DR HSP; P14779; I8U7.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
KW Heme; Monooxygenase; Oxidoreductase.
FT NON_TER 208 208
FT TER 208 208
SQ SEQUENCE 208 AA; 24096 MW; 8254CD4F1CC668C1 CRC64;

Query Match 100.0%; Score 23; DB 3; Length 208;
Best Local Similarity 100.0%; Pred. NO. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 31 EILDV 35

RESULT 35
O95609
ID O95609 PRELIMINARY; PRT; 212 AA.
AC O95609;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fibronectin (Fragment).
GN FN1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Godfrey H.P., Ebrahim A.A.;
RL Submitted (DSC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04850; A000014.1; -.
DR HSSP; P02751; 1FNH.
DR InterPro; IPR003962; FNIII repeat.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; FN3; 1.
DR PRINTS; PR00014; FNTYPIII.
KW Repeat.
FT NON_TER 212 212
FT NON_TER 212 212
SQ SEQUENCE 212 AA; 23232 MW; B3741B219D6B631 CRC64;

Query Match 100.0%; Score 23; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. NO. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 91 EILDV 95

RESULT 36
Q53253
ID Q53253 PRELIMINARY; PRT; 219 AA.
AC Q53253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NodB protein.
GN NODB.
OS Rhizobium tropici.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN299;
RX MEDLINE=97084572; PubMed=8930915;
RA Debelie F., Plazenet C., Roche P., Pujol C., Savagnac A.,
RA Rosenberg C., Prome J.C., Denarie J.;
RT "The NodA proteins of Rhizobium meliloti and Rhizobium tropici specify
the N-acylation of Nod factors by different fatty acids.";
RL Mol. Microbiol. 22:303-314(1996).
DR EMBL; X98514; CAA67138.1; -.
DR InterPro; IPR002509; Polysac_deacet.
DR Pfam; PF01522; Polysac_deacet; 1.
SQ SEQUENCE 219 AA; 23966 MW; 7394719AFFB1743C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. NO. 9.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 38 EILDV 42

RESULT 37
Q9WY98
ID Q9WY98 PRELIMINARY; PRT; 222 AA.
AC Q9WY98;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein TM0260.
GN TM0260.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001708; AAD35348.1; -.
DR TIGR; TM0260; -.
DR InterPro; IPR002727; DUF47.
DR Pfam; PF01865; DUF47; 1.
KW Hypothetical protein; Complete proteome.
```

SQ SEQUENCE 222 AA; 25926 MW; 22B680FFB3CB3B52 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 222;
 Best Local Similarity 100.0%; Pred. No. 9.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 DB 91 EILDV 95

RESULT 38

Q9L6U6 PRELIMINARY; PRT; 226 AA.

AC Q9L6U6; (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative acylhomoserine lactone synthase.
 GN APM1.

OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=BL915;
 RA Flavio A.B., Lam S., Gaffney T.D.;
 RT "Autoinduction regulates production of novel antifungal metabolites in
 RL Pseudomonas fluorescens BL915.";
 DR EMBL; AF232768; AAF61718.1; -;
 DR InterPro; IPR001690; Autoind_synth.
 DR Pfam; PF00765; Autoind_synth; 1.
 DR PRINTS; PR01549; AUTOINDCRSYN.
 DR PRODOM; P0002752; Autoind_synth; 1.
 DR PROSITE; PS00949; AUTOINDUCERS SYNTH; 1.
 SQ SEQUENCE 226 AA; 25922 MW; 99D340438EE95B3D CRC64;

Query Match 100.0%; Score 23; DB 2; Length 226;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 DB 161 EILDV 165

RESULT 39

Q8UA80 PRELIMINARY; PRT; 231 AA.

AC Q8UA80;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein Adu3494.
 GN Adu3494 OR AGR_L 2665.
 OS Agrobacterium tumefaciens (strain CS8 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.

RC MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kucyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RL CS8.";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.

RC MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Quorlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmle K., Gordon J., Vaudin M., Tarchouk O., Epp A., Liu F.,
 RA William C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens CS8.";
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE009279; AAL44307.1; -;
 DR EMBL; AE008333; AAK89900.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 231 AA; 25246 MW; 59110EA68CE538AB CRC64;

Query Match 100.0%; Score 23; DB 16; Length 231;
 Best Local Similarity 100.0%; Pred. No. 9.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 DB 2 EILDV 6

RESULT 40

O27260 PRELIMINARY; PRT; 242 AA.

ID O27260;
 AC O27260;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Conserved protein.
 GN MTH1192.

OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT J. Bacteriol. 179:7135-7155 (1997).
 RL J. Bacteriol. 179:7135-7155 (1997).
 DR EMBL; AB000887; AAB85681.1; -;
 KW Complete proteome.
 SQ SEQUENCE 242 AA; 26475 MW; 8BC1CA2252AE70E2 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 242;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
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 DB 174 EILDV 178

RESULT 41

Q9FDJ6 PRELIMINARY; PRT; 246 AA.

ID Q9FDJ6

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AC Q9FDJ6; 2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Hypothetical 28.8 kDa protein.
GN E25B.
OS Lactobacillus rhamnosus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Lactobacillaceae; Lactobacillus.
OX NCBI_TaxID=47715;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X202;
RA Grimaldi C., Dutertre M., Simonet J.M.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF238861; AAG01982.1; -.
KW Hypothetical protein.
SQ SEQUENCE 246 AA; 28789 MW; EA82CCE2178252AF CRC64;

Query Match 100.0%; Score 23; DB 2; Length 246;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 124 EILDV 128

RESULT 42
Q8XE09
ID Q8XE09 PRELIMINARY; PRT; 250 AA.
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Orf, hypothetical protein.
GN Z3503 OR ECS3130.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Apodaca E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Welch R.A., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Ikeda T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22 (2001).
DR EMBL; AE005457; AAG57376.1; -.
DR EMBL; AP002561; BAB36553.1; -.
DR InterPro; IPR005000; HPC_Hpai.
DR Pfam; PF03328; HpcH_Hpai; 1.
KW Complete proteome.
SQ SEQUENCE 250 AA; 26948 MW; 423FFFC817975600 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 250;
Best Local Similarity 100.0%; Pred. No. 1e+03;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 146 EILDV 150

RESULT 43
O51655
ID O51655 PRELIMINARY; PRT; 253 AA.
AC O51655;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BB0713.
GN BB0713.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi."
RL Nature 390:580-586 (1997).
DR EMBL; AE001171; AAC67060.1; -.
DR TIGR; BB0713; -.
DR InterPro; IPR003743; DUF164.
DR Pfam; PF02591; DUF164; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 29838 MW; 20169A5790F824E1 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 125 EILDV 129

RESULT 44
O44520
ID O44520 PRELIMINARY; PRT; 256 AA.
AC O44520;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE H10D12.2 protein.
GN H10D12.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Korshaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

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QY 1 EILDV 5
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Db 156 EILDV 160

RESULT 48

O24845 ID O24845 PRELIMINARY; PRT; 270 AA.

AC O24845; 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 30.5 kDa protein.
OS Acinetobacter sp. ADP1.
OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae;
OC Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=ADP1;
RX MEDLINE=99287833; PubMed=10348863;
RA Segura A., Bunz P.V., D'Argenio D.A., Ornston L.N.;
RT "Genetic analysis of a chromosomal region containing vanA and vanB,
RT genes required for conversion of either ferulate or vanillate to
RT protocatechuate in Acinetobacter.";
RL J. Bacteriol. 181:3494-3504(1999).
CC -1- SIMILARITY: BELONGS TO THE ICLR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.

DR EMBL: AF009672; AAC27111.1; -;
DR InterPro: IPR000285; HTH_ICLR.

DR Pfam: PF01614; ICLR; 1.
DR SMART: SM00346; HTH_ICLR; 1.

KW DNA-binding; Hypothetical protein; Transcription regulation.
SQ SEQUENCE 270 AA; 30524 MW; DB457B57BF817FBC CRC64;

Query Match 100.0%; Score 23; DB 2; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
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|
|
Db 50 EILDV 54

RESULT 49

Q9H027 ID Q9H027 PRELIMINARY; PRT; 271 AA.

AC Q9H027; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 30.5 kDa protein.
GN DFXP761J139.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=AMYGDALA;
RA Blum H., Bauersachs S., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL512712; CAC21654.1; -;
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; zf-CCHC; 4.
DR SMART: SM00343; Znf_C2HC; 4.
KW Hypothetical protein.
SQ SEQUENCE 271 AA; 30477 MW; D68EDABE8B9D0F3D CRC64;

Query Match 100.0%; Score 23; DB 4; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
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Db 251 EILDV 255

RESULT 50

Q9EQ23 ID Q9EQ23 PRELIMINARY; PRT; 274 AA.

AC Q9EQ23; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE C-kit receptor (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BROWN NORWAY; TISSUE=TESTIS;
RA Gangadharan S., Ali S.;

RT "RT-PCR generated mRNA transcript of c-kit (encompassing extracellular
RT domain) originating from testis of 1 day old rat";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF296694; AAG48585.1; -;
DR InterPro: IPR003600; IG_like.
DR SMART: SM00410; IG_like; 1.
KW Receptor.
FT NON_TER. 274 274

SQ SEQUENCE 274 AA; 30507 MW; 00FA042B09D0103 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
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Db 69 EILDV 73

RESULT 51

Q921S2 ID Q921S2 PRELIMINARY; PRT; 277 AA.

AC Q921S2; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to DnaJ (Hsp40) homolog, subfamily B, member 10.
GN DNAJB10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC011090; AAH11090.1; -;
DR MGD; MGI:1928739; DnaJb10.
DR InterPro: IPR001623; DnaJ N.
DR InterPro: IPR002950; Josephin.
DR InterPro: IPR003903; UIM.
DR Pfam: PF00226; DnaJ; 1.
DR Pfam: PF02809; UIM; 2.
DR PROSITE: PS00636; DNAJ_1; UNKNOWN_1.
DR PROSITE: PS00076; DNAJ_2; 1.

SQ SEQUENCE 277 AA; 30675 MW; 6D9198A5C4FA1DA3 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5

Db 6 EILDV 10
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RESULT 52

Q52412 Q52412 PRELIMINARY; PRT; 282 AA.
ID AC Q52412; Q52409;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TF1-gamma subunit.
OS thermophilic bacterium PS3.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales.
OX NCBI_TaxID=2334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8816379; PubMed=2894854;
RA Ohta S., Yoshida M., Ishizuka M., Hirata H., Hamamoto T.,
RA Otawara-Hamamoto Y., Matsuda K., Kagawa Y.;
RT "Sequence and over-expression of subunits of adenosine triphosphate
synthase in thermophilic bacterium PS3."
RL Biochim. Biophys. Acta 933:141-141(1988).
[2]
RP SEQUENCE OF 273-282 FROM N.A.
RC STRAIN=PS3;
RX MEDLINE=87137359; PubMed=2880841;
RA Kagawa Y., Ishizuka M., Saitoh T., Nakao S.;
RT "Stable structure of thermophilic proton ATPase beta subunit."
RL J. Biochem. 100:923-934(1986).
DR EMBL; X07804; CAA30654.1; -
DR EMBL; D00113; BAA00065.1; -
DR EMBL; X04609; CAA28276.1; -
DR InterPro; IPR000131; ATPase_gamma.
DR Pfam; PF00231; ATP-synt; 1.
DR PRINTS; PR00126; ATPSEGAMMA.
DR TIGRfam; TIGR01146; ATPSV1_Figamma; 1.
DR PROSITE; PS00153; ATPASE_GAMMA; 1.
SQ SEQUENCE 282 AA; 31778 MW; FA17CE9482EE9F7 CRC64;

Query Match 100.0%; Score 23; DB 23; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 208 EILDV 212

RESULT 53

Q8TJNO Q8TJNO PRELIMINARY; PRT; 285 AA.
ID AC Q8TJNO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Predicted protein.
GN MA3750.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity."
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011086; AAM07103.1; -
KW Complete proteome.
SQ SEQUENCE 285 AA; 32209 MW; 9AEBDB37DA8868F5 CRC64;

Query Match 100.0%; Score 23; DB 17; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 127 EILDV 131

RESULT 54

Q9CN70 Q9CN70 PRELIMINARY; PRT; 287 AA.
ID AC Q9CN70;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein PM0569.
GN PM0569.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PM70;
RX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida PM70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
DR EMBL; AE006092; AAK02653.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 287 AA; 32697 MW; C702D786DE56853B CRC64;

Query Match 100.0%; Score 23; DB 16; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||

Db 202 EILDV 206

RESULT 55

O17829 O17829 PRELIMINARY; PRT; 290 AA.
ID AC O17829;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F21A3.3 protein.
GN F21A3.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurray A.A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 investigating biology."
 RL Science 282:2012-2018(1998).
 DR EMBL; Z81509; CAB04157.1; -.
 DR InterPro; IPR000561; EGF-like.
 DR SMART; SMART03582; SHKT.
 DR SMART; SMART0181; EGF; 1.
 DR SMART; SMART0254; SHKT; 1.
 DR PROSITE; PS00022; EGF 1; UNKNOWN 1.
 SQ SEQUENCE 290 AA; 35686 MW; 700F9B8E1365687F CRC64;

Query Match 100.0%; Score 23; DB 5; Length 290;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 150 EILDV 154

RESULT 56

Q8RLZ4 PRELIMINARY; PRT; 304 AA.

AC Q8RLZ4
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE N-acetylneuraminic acid synthase.
 GN SIAA.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OC NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2019;
 RX PubMed=118442084;
 RA Jones P.A., Samuels N.M., Phillips N.J., Munson R.S. Jr., Bozue J.A.,
 RA Arseneau J.A., Nichols W.A., Zaleski A., Gibson B.W., Apicella M.A.;
 RT "Haemophilus influenzae Type b Strain A2 Has Multiple
 RT Sialyltransferases Involved in Lipooligosaccharide Sialylation."
 RL J. Biol. Chem. 277:14598-14611(2002).
 DR EMBL; AY061634; AAL38659.1; -.
 SQ SEQUENCE 304 AA; 36115 MW; 49645B793FFBDF90 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 304;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 255 EILDV 259

RESULT 57

Q9JUD6 PRELIMINARY; PRT; 307 AA.

AC Q9JUD6
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative sulphate adenylate transferase subunit 2 (EC 2.7.7.4).
 GN CYSD OR NMA1365.
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID=65699;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis Z2491".
 RL Nature 404:502-506(2000).
 DR EMBL; AL162755; CAB84611.1; -.
 DR InterPro; IPR002500; PAPS_reduct.
 DR Pfam; PF01507; PAPS_reduct; 1.
 KW Transferase; Nucleotidyltransferase; Complete proteome.
 SQ SEQUENCE 307 AA; 34724 MW; 6D2A1E060C31124C CRC64;

Query Match 100.0%; Score 23; DB 16; Length 307;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 244 EILDV 248

RESULT 58

Q9JS34 PRELIMINARY; PRT; 307 AA.

AC Q9JS34
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Sulfate adenyltransferase, subunit 2.
 GN NMB1192 AND NMB1154.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OC NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignani V., Pizsa M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58".
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002467; AAF41575.1; -.
 DR EMBL; AE002464; AAF41540.1; -.
 DR TIGR; NMB1154; -.
 DR TIGR; NMB1192; -.
 DR InterPro; IPR002500; PAPS_reduct.
 DR Pfam; PF01507; PAPS_reduct; 1.
 KW Transferase; Nucleotidyltransferase; Complete proteome.
 SQ SEQUENCE 307 AA; 34696 MW; 4BFF5DB3861D0FD3 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 307;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 244 EILDV 248

RESULT 59

Q9X9K3 PRELIMINARY; PRT; 308 AA.

AC Q9X9K3
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chemotaxis Chev homolog.
GN CHEV
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BB22;
RA McCarter L.L.;
RT "Polar Flagellar Region I.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12817; AAD42910.1; -.
DR HSSP; P06143; 1AB6.
DR InterPro; IPR002545; Response_reg.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF01584; Chew; 1.
DR Pfam; PF00072; response reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00260; Chew; 1.
DR SMART; SM00448; REC; 1.
KW Phosphorylation; Sensory transduction.
SQ SEQUENCE 308 AA; 34126 MW; 5E21A365839BB978 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 145 EILDV 149

RESULT 60
O74864
ID O74864 PRELIMINARY; PRT; 312 AA.
AC
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Putative 60s acidic ribosomal protein p0.
GN SPC18.14C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Hilbert H.; Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031907; CAA21428.1; -.
DR InterPro; IPR001813; 60s.ribosomal.
DR InterPro; IPR001790; Ribosomal L10.
DR Pfam; PF00428; 60s.ribosomal; 1.
DR Pfam; PF00466; Ribosomal_L10; 1.
KW Ribosomal protein.
SQ SEQUENCE 312 AA; 33565 MW; 68979A46B921F761 CRC64;

Query Match 100.0%; Score 23; DB 3; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 200 EILDV 204

RESULT 61
Q8R342
ID Q8R342 PRELIMINARY; PRT; 314 AA.
AC Q8R342;
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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to protein phosphatase 2, regulatory subunit B (B56), beta
DE isoform (fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026670; AAH26670.1; -.
FT NON_TER 1
SQ SEQUENCE 314 AA; 36619 MW; BF6F70007B3E9081 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 314;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 158 EILDV 162

RESULT 62
Q9GMV1
ID Q9GMV1 PRELIMINARY; PRT; 317 AA.
AC
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 35.5 kDa protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN PARIETAL LOBE;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain CDNA
RT libraries.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB047624; BAB12148.1; -.
DR HSSP; P56536; 2KIN.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1.
DR PRINTS; PR00380; KINESINHEAVY.
DR SMART; SM00129; KISC; 1.
DR PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.
DR PROSITE; PS00667; KINESIN MOTOR DOMAIN2; 1.
KW ATP-binding; Coiled coil; Hypothetical protein; Microtubules;
KW Motor protein.
SQ SEQUENCE 317 AA; 35489 MW; 28FDC60C4F75A684 CRC64;

Query Match 100.0%; Score 23; DB 6; Length 317;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 74 EILDV 78

RESULT 63
Q97PFO
ID Q97PFO PRELIMINARY; PRT; 321 AA.
AC Q97PFO;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
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DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Pyridine nucleotide-dialdehyde oxidoreductase family
 DE protein.
 GN SPI563.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TTGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Winn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapfel E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson J.C.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae";
 RL Science 293:498-506(2001).
 DR EMBL; AB007451; AAK75650.1; -;
 DR TIGR; SPI563; -;
 DR InterPro; IPR000759; Adnrdx reductase.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR000103; Pyridine redox_2.
 DR InterPro; IPR001100; Pyr_redox.
 DR Pfam; PF00070; Pyr_redox; 1.
 DR PRINTS; PR00419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00411; PNDRDTASEI.
 DR PRINTS; PR00469; PNDRDTASEII.
 KW Complete proteome.
 KW SEQUENCE 321 AA; 35141 MW; FF89A0B001BD8452 CRC64;
 SQ
 Query Match 100.0%; Score 23; DB 16; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 51 EILDV 55
 ID Q99W56 PRELIMINARY; PRT; 321 AA.
 AC Q99W56;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical protein SAV0553.
 GN SAV0553 OR SA0511.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcaceae.
 OX NCBI_TaxID=158878; 158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPICIS=S.aureus (strain Mu50), and S.aureus (strain N315);
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iijima J.-O., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiranatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003359; BAB56715.1; -;
 DR EMBL; AP003130; BAB41742.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 321 AA; 36053 MW; E0B08B19CF630CB0 CRC64;
 Query Match 100.0%; Score 23; DB 16; Length 321;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 50 EILDV 54
 ID Q9RJ06 PRELIMINARY; PRT; 322 AA.
 AC Q9RJ06;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Putative RNA polymerase sigma factor.
 GN SC00159 OR SCJ1.08.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=970000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 RT coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
 CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
 CC THEN IS RELEASED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY. ECF SUBFAMILY.
 DR EMBL; AL109962; CAB53126.1; -;
 DR InterPro; IPR000838; Sigma70_ECF.
 DR Pfam; PF00776; Sigma70_ECF; 1.
 KW DNA-binding; DNA-directed RNA polymerase; Sigma factor;
 KW Transcription regulation.
 SQ SEQUENCE 322 AA; 35466 MW; C4E8BA53849677D CRC64;

Query Match 100.0%; Score 23; DB 16; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
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|
|
Db 148 EILDV 152

RESULT 66

ID Q96F52 PRELIMINARY; PRT; 324 AA.
AC Q96F52;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DnaJ (Hsp40) homolog, subfamily B, member 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LYMPH;
RA Strauberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011609; AAH11609.1; -.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR002950; Josephin.
DR InterPro; IPR001230; Prenyl_site.
DR InterPro; IPR003903; UIM.
DR Pfam; PF00226; DnaJ; 1.
DR Pfam; PF02809; UIM; 2.
DR PROSITE; PS00636; DNAJ_1; UNKNOWN_1.
DR PROSITE; PS00076; DNAJ_2; 1.
DR PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
SQ SEQUENCE 324 AA; 35580 MW; 0154ED3E29F34B4A CRC64;

Query Match 100.0%; Score 23; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
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|
|
Db 6 EILDV 10

RESULT 67

ID Q25779 PRELIMINARY; PRT; 324 AA.
AC Q25779;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Thioredoxin reductase (TRXB).
GN HPI164.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Peterson S.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Clodek A.,
RA McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg O.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,

RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AE000622; AAD08209.1; -.
DR TIGR; HPI164; -.
DR InterPro; IPR001327; FAD_pyr_redox.
DR Pfam; PF00070; pyr_redox; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 324 AA; 35986 MW; 0854598651D92B30 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
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|
|
Db 4 EILDV 8

RESULT 68

ID Q9ZKS1 PRELIMINARY; PRT; 324 AA.
AC Q9ZKS1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative thioredoxin reductase.
GN TRXB_2 OR JHP1091.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
ON NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999).
CC -1- COFACTOR: FAD (BY SIMILARITY).
DR EMBL; AE001536; AAD06662.1; -.
DR InterPro; IPR000759; Adrndx reductase.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR000103; Pyridine_redox_2.
DR InterPro; IPR001100; pyr_redox.
DR Pfam; PF00070; pyr_redox; 1.
DR PRINTS; PR00419; ADXRDTASE.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNDRTASEI.
DR PRINTS; PR00469; PNDRTASEII.
KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 324 AA; 36006 MW; 27BC82CAll19E320 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 324;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
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Db 4 EILDV 8

RESULT 69

ID O28580 PRELIMINARY; PRT; 329 AA.
AC O28580;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Phosphoribosylformylglycinamide cyclo-ligase (PURM).
 GN AF1693.
 OS Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 Richardson D.L., Kervagadash J., Lee N.H., Sutton G.G., Gill S.,
 Fleischmann R.D., Clavagenush J., Adams M.D., Loftus B.,
 Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
 Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 Venter J.C.;
 RA "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE000986; AA889555.1; -.
 DR HSP; P08178; 1CL1.
 DR TIGR; AF1693; -.
 DR InterPro; IPR000728; AIRS related.
 DR InterPro; IPR004733; PurM_Cligase.
 DR Pfam; PF00586; AIRS; 1.
 DR Pfam; PF02769; AIRS; C; 1.
 DR TIGRFAMS; TIGR00878; purM; 1.
 KW Hypothetical protein; Ligase; Complete proteome.
 SQ SEQUENCE 329 AA; 36209 MW; C9D291148AE3DD34 CRC64;

 Query Match 100.0%; Score 23; DB 17; Length 329;
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 BILDV 5
 DB 222 EILDV 226

 RESULT 70
 Q9PR68 PRELIMINARY; PRT; 333 AA.
 AC Q9PR68
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein U0077.
 GN U0077;
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SERVAR 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
 Cassell G.H.;
 RA "The complete sequence of the mucosal pathogen Ureaplasma
 urealyticum";
 RL Nature 407:757-762(2000).
 DR EMBL; AE002107; AAF30482.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 333 AA; 40137 MW; 39BD610454AD6985 CRC64;

 Query Match 100.0%; Score 23; DB 16; Length 333;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;

 QY 1 BILDV 5
 DB 222 EILDV 226

 RESULT 71
 Q8YU24 PRELIMINARY; PRT; 337 AA.
 ID Q8YU24
 AC Q8YU24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein Alr2187.
 GN ALR2187.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 Yasuda M., Tabata S.;
 RA "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003588; BAB73886.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 337 AA; 39125 MW; 9E6A546CFEFP6BB CRC64;

 Query Match 100.0%; Score 23; DB 16; Length 337;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 BILDV 5
 DB 212 EILDV 216

 RESULT 72
 Q97CD7 PRELIMINARY; PRT; 338 AA.
 ID Q97CD7
 AC Q97CD7;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Phosphoribosylformylglycinamide cyclo-ligase.
 GN TV0165 OR TVG0175535.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=50339;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
 RX MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 Kawashima T., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
 Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RA "Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL; AP000991; BAB59307.1; -.
 DR InterPro; IPR000728; AIRS related.
 DR InterPro; IPR004733; PurM_Cligase.
 DR Pfam; PF00586; AIRS; 1.
 DR Pfam; PF02769; AIRS; C; 1.
 DR TIGRFAMS; TIGR00878; purM; 1.
 KW Ligase; Complete proteome.

SQ SEQUENCE 338 AA; 37183 MW; 0AC488696971DEP5 CRC64;
 Query Match 100.0%; Score 23; DB 17; Length 338;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 DB 223 EILDV 227

RESULT 73
 Q93HG3 PRELIMINARY; PRT; 339 AA.
 ID Q93HG3
 AC Q93HG3
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 3-oxoacyl-(acyl carrier protein) synthase III.
 OS Streptomyces avermitilis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: Deducing the ability of producing secondary
 RT metabolites";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 DR EMBL; AB070943; BAB69224.1; -;
 SQ SEQUENCE 339 AA; 36249 MW; EIC24B1D9665CD87 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 339;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 DB 332 EILDV 336

RESULT 74
 Q57369 PRELIMINARY; PRT; 344 AA.
 ID Q57369
 AC Q57369
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Flagellar switch protein.
 GN FLAG.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=212;
 RA Ge Y., Saint Girons I., Old I., Charon N.W.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=212;
 RC MEDLINE=96186958; PubMed=8626068;
 RA Ge Y., Old I., Saint Girons I., Yelton D.B., Charon N.W.;
 RT "Flh and flh of Borrelia burgdorferi are similar to flagellar and
 RT virulence factor export proteins of other bacteria";
 RL Gene 168:73-75(1996).
 DR EMBL; L76303; AAB51411.1; -;
 DR EMBL; U09711; AAB41945.1; -;
 DR HSSP; Q9WY63; 1QC7.

DR InterPro; IPR000090; Flg_Motor_Flg.
 DR Pfam; PF01706; Flg-C_1.
 DR PRINTS; PRO0954; FLMOTORFLIG.
 DR TIGRFAMS; TIGR00207; Flg; 1.
 KW Flagella.
 SQ SEQUENCE 344 AA; 39018 MW; 07B0353EC7F43FFD CRC64;
 Query Match 100.0%; Score 23; DB 2; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 DB 8 EILDV 12

RESULT 75
 Q8V3G8 PRELIMINARY; PRT; 344 AA.
 ID Q8V3G8
 AC Q8V3G8
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE SPV128 hydroxysteroid dehydrogenase-like protein.
 GN SPV128.
 OS Swinepox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Suipoxvirus.
 OX NCBI_TaxID=10276;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17077-99;
 RX MEDLINE=21624277; PubMed=11752168;
 RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Osorio F.A., Balinsky C.,
 RA Kutish G.F., Rock D.L.;
 RT "The genome of swinepox virus";
 RL J. Virol. 76:783-790(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17077-99;
 RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C., Osorio F.A., Zsak L.,
 RA Kutish G.F., Rock D.L.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF410153; AAL69867.1; -;
 DR InterPro; IPR002225; 3Beta_HSD.
 DR InterPro; IPR000977; DNA_ligase.
 DR Pfam; PF01073; 3Beta_HSD; 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN 1.
 SQ SEQUENCE 344 AA; 39342 MW; ECD2B807E7EDE018 CRC64;
 Query Match 100.0%; Score 23; DB 12; Length 344;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 DB 89 EILDV 93

Search completed: February 8, 2003, 10:24:41
 Job time : 34 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:19:43 ; Search time 35 Seconds
(without alignments)
19.036 Million cell updates/sec

Title: US-09-251-073A-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 249

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_101002.*
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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	5	17	AA95719
2	23	100.0	5	18	AA25192
3	23	100.0	5	19	AA46318
4	23	100.0	5	20	AAV03855
5	23	100.0	5	21	AAV80488
6	23	100.0	5	21	AAV77442
7	23	100.0	5	21	AAV69619
8	23	100.0	5	22	AA873465
9	23	100.0	5	22	AA891966
10	23	100.0	5	22	AA50876

11	23	100.0	5	22	AA559135	Peptide #3 recogni
12	23	100.0	6	21	AAV77443	Fibronectin CSI-de
13	23	100.0	6	21	AAV77444	Fibronectin CSI-de
14	23	100.0	7	19	AA56065	Alpha4 integrins t
15	23	100.0	8	12	AA811361	Peptide #352 deriv
16	23	100.0	8	13	AA828885	Cell adhesion inh
17	23	100.0	8	13	AA844360	Polymer-bound cell
18	23	100.0	8	17	AA92536	VLA-4 binding pept
19	23	100.0	8	18	AAW25190	LDV-peptide capabl
20	23	100.0	8	19	AAW63133	Peptide sequence o
21	23	100.0	8	19	AAW56046	Chimeric adenoviru
22	23	100.0	8	20	AAV32862	Fibronectin protei
23	23	100.0	8	20	AAV32862	Fibronectin protei
24	23	100.0	8	21	AA835734	Vitronectin peptid
25	23	100.0	8	21	AAV80489	Cell adhesion pept
26	23	100.0	8	21	AAV69618	VLA-4 inhibitor pe
27	23	100.0	8	22	AA873464	Fibronectin VLA-4
28	23	100.0	8	22	AA891967	Fibronectin fragme
29	23	100.0	9	13	AA829631	Adhesion inhibitor
30	23	100.0	9	13	AA830433	Cell adhesion inh
31	23	100.0	9	13	AA828886	Cell adhesion inh
32	23	100.0	9	21	AAV77436	Fibronectin CSI-de
33	23	100.0	9	21	AAV77437	Fibronectin CSI-de
34	23	100.0	9	21	AAV77438	Fibronectin CSI-de
35	23	100.0	9	21	AAV77439	Fibronectin CSI-de
36	23	100.0	10	13	AA825998	Adhesion inhibitor
37	23	100.0	10	13	AA830432	Cell adhesion inh
38	23	100.0	10	13	AA829103	Platelet aggregati
39	23	100.0	10	13	AA829105	Platelet aggregati
40	23	100.0	10	13	AA829106	Platelet aggregati
41	23	100.0	10	13	AA829107	Platelet aggregati
42	23	100.0	10	13	AA829108	Platelet aggregati
43	23	100.0	10	13	AA829109	Platelet aggregati
44	23	100.0	10	16	AAW01705	Standard peptide f
45	23	100.0	10	16	AAW01725	Inhibitor of fibro
46	23	100.0	10	17	AA895804	Alpha-4beta-1 inte
47	23	100.0	10	19	AAW70543	CS-1 peptide fragm
48	23	100.0	10	19	AAW71246	Peptide sequence o
49	23	100.0	10	20	AAW88058	CS-1 peptide porti
50	23	100.0	10	21	AAV77412	Fibronectin CSI-de
51	23	100.0	10	21	AAV74984	Transfection asoc
52	23	100.0	10	23	AA817114	Integrin-binding p
53	23	100.0	11	17	AA825355	VLA-4 binding pept
54	23	100.0	12	16	AAW01704	B12 peptide sequen
55	23	100.0	12	20	AAW88061	Integrin-binding p
56	23	100.0	12	20	AAW95414	Fibronectin CSI-de
57	23	100.0	12	21	AAV77411	Non-RGD containing
58	23	100.0	12	23	AAU74966	Integrin-binding p
59	23	100.0	12	23	AA817104	CS-1 peptide seque
60	23	100.0	13	19	AAW70541	Peptide sequence o
61	23	100.0	13	19	AAW71245	SEQ ID 57 of WO992
62	23	100.0	13	20	AAV22632	Synthetic CS-1 pep
63	23	100.0	13	22	AA870883	Very late antigen-
64	23	100.0	13	23	AAU77526	Human HSJ1 immunog
65	23	100.0	15	23	AAU98858	Adhesion inhibitor
66	23	100.0	16	13	AA829632	Platelet aggregati
67	23	100.0	16	13	AA829104	Laminin-related pe
68	23	100.0	19	23	AAU81181	Laminin-related pe
69	23	100.0	19	23	AAU81184	Laminin-related pe
70	23	100.0	19	23	AAU81185	Laminin-related pe
71	23	100.0	20	13	AA826821	Cell adhesion poly
72	23	100.0	20	13	AA830901	Cell adhesion poly
73	23	100.0	20	19	AAW56047	Chimeric adenoviru
74	23	100.0	21	19	AAW56064	Alpha4 integrins t
75	23	100.0	23	20	AAV13421	Conjugated control
76	23	100.0	24	16	AA867898	Control peptide to
77	23	100.0	25	13	AA820498	CS1 peptide. Synt
78	23	100.0	25	15	AA856245	Fibronectin-derive
79	23	100.0	25	15	AA859382	Fibronectin fragme
80	23	100.0	25	16	AAW01703	Fibronectin recogn
81	23	100.0	25	16	AA882248	CS-1 cell binding
82	23	100.0	25	16	AA883684	33 KD fibronectin
83	23	100.0	25	17	AA898813	Cell adhesion suba

84 23 100.0 25 18 AAW33337 Human fibronectin
 85 23 100.0 25 18 AAW21690 IIICS binding doma
 86 23 100.0 25 20 AAY32863 Fibronectin protei
 87 23 100.0 25 20 AAY32875 Fibronectin protei
 88 23 100.0 25 20 AAW80857 CS-1 peptide whose
 89 23 100.0 25 20 AAW81844 Fibronectin-like p
 90 23 100.0 25 21 AAW77410 Fibronectin CS1-de
 91 23 100.0 25 21 AAY78584 Fibronectin derive
 92 23 100.0 25 23 AAE23649 Human fibronectin
 93 23 100.0 25 23 AAU74672 Human fibronectin
 94 23 100.0 25 23 AAU81174 Lamamin related pe
 95 23 100.0 26 13 AAR30902 Cell adhesion poly
 96 23 100.0 26 20 AAY52099 Peptide containing
 97 23 100.0 26 20 AAY13416 Conjugated control
 98 23 100.0 26 22 AAB48439 Fibronectin CS1 se
 99 23 100.0 26 22 AAB49890 Fibronectin CS1 se
 100 23 100.0 26 23 ABB77881 CS1 sequence of fi

ALIGNMENTS

RESULT 1
 AAR95719
 ID AAR95719 standard; peptide; 5 AA.

XX AC AAR95719;

XX DT 04-DEC-1996 (first entry)

XX DE Alpha-4Beta-1 integrin binding inhibitory peptide 16.

XX KW VCAM-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
 XX KW inhibitor; binding; white blood cell; migration; capillary wall;
 XX KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
 XX KW CS1; CS5; HI; LDV; active site.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Modified-site 5
 XX FT /note= "Val-NH2"

XX PN US5510332-A.

XX PD 23-APR-1996.

XX XX 07-JUL-1994; 94US-0271830.

XX XX 07-JUL-1994; 94US-0271830.

XX PA (TEXA-) TEXAS BIOTECHNOLOGY CORP.

XX XX Beck PJ, Kogan TP, Ren K, Vanderslice P;

XX XX WPI; 1996-221274/22.

XX FT New peptide(s) based on the LDV domain of fibronectin - used for
 XX FT inhibiting binding of alpha-4, beta-1 integrin to VCAM-1,
 XX FT fibronectin or invasin

XX PS Disclosure; Column 21-22; 35pp; English.

XX CC Vascular cell adhesion molecule-1 (VCAM-1) is protein found on the
 XX CC surface of endothelial cells that line the interior wall of capillaries.
 XX CC VCAM-1 recognizes and binds to the integrin alpha-4beta-1 (IA4B1; or
 XX CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
 XX CC surface of certain white blood cells. Binding of IA4B1 to VCAM-1 allows
 XX CC white blood cells to adhere to the capillary wall in areas where the
 XX CC tissue surrounding the capillary has been infected or damaged. Sometimes
 XX CC this white blood cell migration can become uncontrolled, with white
 XX CC blood cells flooding to the scene, causing widespread tissue damage.
 XX CC Cpd. capable of blocking this process may be beneficial as therapeutic

CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
 CC fibronectin. Three distinct IA4B1-binding sites have been identified
 CC within fibronectin. One site is found in the HepII region and is
 CC expressed in all isoforms; two others (CS1 and CS5) are present in the
 CC alternatively spliced type III connecting segments. CS1 has the higher
 CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
 CC site. Peptides AAR95704-805 are modeled after a portion of the CS1
 CC peptide that include the LDV domain presented in such a way by its novel
 CC flanking sequence to produce a potent inhibitor of IA4B1 binding.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 17; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5

Db 1 EILDV 5

RESULT 2

AAW25192

ID AAW25192 standard; peptide; 5 AA.

XX AC AAW25192;

XX DT 05-JAN-1998 (first entry)

XX DE LDV-peptide capable of binding cell adhesion molecules.

XX KW LDV; leucine; aspartic acid; valine; cell adhesion molecule;
 XX KW binding; bladder irrigation; tumour removal; endoscopic operation;
 XX KW transurethral resection; cancer; neoplasia.

XX OS Synthetic.

XX PN DE19529909-A1.

XX PD 20-FEB-1997.

XX PF 15-AUG-1995; 95DE-1029909.

XX PR 15-AUG-1995; 95DE-1029909.

XX XX (PREP) FRESENIUS AG.

XX PA Boehle A;

XX XX WPI; 1997-133793/13.

XX FT Endoscopic irrigation solns. - contg. peptide(s) that bind to cell
 XX FT adhesion molecules

XX PS Claim 6; Page 8; 8pp; German.

XX CC AAW25187-W25192 are peptides containing an LDV sequence or equivalent.
 XX CC The peptides are capable of binding to cell adhesion molecules and
 XX CC are used in aqueous irrigation solutions for use during and after
 XX CC endoscopic operations. Preferred irrigation solutions are
 XX CC electrolyte-free and contain 1 microg/ml to 100 mg/ml of one or more
 XX CC oligopeptides containing the amino acid sequences: RGD, LDV, IDA, DGEA,
 XX CC GPRP, VIL, YIGSR, KQAGDV and/or REDV (given in one letter amino acid
 XX CC code). The solutions are especially used for irrigating the bladder
 XX CC during and after tumour removal by transurethral resection. The
 XX CC peptides protect against recurrence of tumours.

XX SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 18; Length 5;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 1 EILDV 5

RESULT 3

AAW46318
 ID AAW46318 standard; Protein; 5 AA.

XX AAW46318;
 AC

XX 08-MAY-1998 (first entry)
 DT

XX Peptide recognised by integrin alpha4etal.
 DE

XX Fibrinogen; integrin; alpha-IIB-beta3; cell surface receptor;
 KW penton base protein; coat proteins; adenovirus; binding site;
 KW cellular adhesion; extracellular matrix molecule; binding domain;
 KW cell surface binding site; bispecific molecule; gene therapy.
 XX

OS Unidentified.

XX US5712136-A.
 PN

XX 27-JAN-1998.
 PD

XX 17-APR-1996; 96US-0634060.
 PF

XX 08-SEP-1994; 94US-0303162.
 PR

XX (GENV-) GENVEC INC.
 PA

XX Brough DE, Bruder JT, Kovesdi I, McVey DL, Roelvink PW;
 PI Wickham TJ;

XX WPI; 1998-119984/11.
 DR

XX Methods for introducing adenovirus into cells - used for genetic
 PT engineering and gene therapy

XX Claim 27; Column 2; 56pp; English.
 PS

XX The present sequence is a linear stretch of amino acids (present in
 CC fibronectin) recognised by the integrin alpha4beta1. Integrins are
 CC cell surface receptors. The penton base protein (one of the coat
 CC proteins) of adenoviruses binds to integrins. The integrins not only
 CC provide a binding site for the adenoviral penton base protein, but also
 CC mediate cellular adhesion to the extracellular matrix molecules. The
 CC specification describes a method of introducing an adenovirus into
 CC a cell in vitro having a particular cell surface binding site. The
 CC adenovirus is contacted with a bispecific molecule comprising a component
 CC that selectively binds a binding domain of the penton base protein of the
 CC adenovirus and a second component that selectively binds the cell surface
 CC binding site. A complex of the adenovirus and the bispecific molecule is
 CC formed, and the cell is contacted with it to allow entry of the
 CC adenovirus into the cell. The methods can be used for research and the
 CC vectors can be used for gene therapy.

SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 1 EILDV 5

RESULT 4

AAW03855
 ID AAW03855 standard; peptide; 5 AA.

XX

AC AAY03855;

XX 16-JUN-1999 (first entry)
 DT

XX Integrin ligand dissociator (ILD) peptide.
 DE

XX Integrin-ligand; dissociator; disaggregation; platelet thrombus; stroke;
 KW fibrinogen; glycoprotein IIB-IIIA; angina; myocardial infarction; bone;
 KW osteoclast; osteoporosis; angiogenesis; cancer; diabetic retinopathy;
 KW psoriasis; tumour; atherosclerosis; inflammatory bowel disease; asthma;
 KW organ transplant rejection; arthritis; ILD.

XX Synthetic.
 OS

XX WO9911280-A1.
 PN

XX 11-MAR-1999.
 PD

XX 03-SEP-1998; 98WO-US18305.
 PF

XX 03-SEP-1997; 97US-0057463.
 PR

XX (BURN-) BURNHAM INST.
 PA

XX Hu DD, Smith JW;
 PI

XX WPI; 1999-243586/20.
 DR

XX Disaggregating a ligand: integrin receptor complex
 PT

XX Disclosure; Page 10; 39pp; English.
 PS

XX The invention relates to integrin ligand dissociators. Disaggregation of
 CC an existing platelet thrombus in a blood vessel is due to dissociation of
 CC fibrinogen from glycoprotein IIB-IIIA. This dissociation is caused by the
 CC binding of an integrin-ligand dissociator at ligand binding site I of
 CC glycoprotein IIB-IIIA. The invention provides a method of disaggregating
 CC an existing platelet thrombus in a blood vessel, where the platelet
 CC thrombus may form an occlusion of a blood vessel, in a subject comprising
 CC administering a compound which dissociates fibrinogen bound to a first
 CC site on platelet glycoprotein IIB-IIIA, by binding to a second
 CC interacting site on platelet glycoprotein IIB-IIIA, disaggregating the
 CC platelet thrombus. The method is used to treat humans with unstable
 CC angina, stroke and/or acute myocardial infarction. The methods can be
 CC used to enact de-adhesion of osteoclasts from the bone surface to halt
 CC bone loss in a patient with osteoporosis. The methods can also be used
 CC for the de-adhesion of angiogenic endothelial cells in a patient with a
 CC pathologic condition associated with angiogenesis, e.g. cancer, diabetic
 CC retinopathy, psoriasis. The methods can also be used to treat tumours,
 CC atherosclerosis, inflammatory conditions, e.g. arthritis, inflammatory
 CC bowel disease, or organ transplant rejection, and asthma. The methods can
 CC be used for the dissolution of pre-formed platelet aggregates, which is a
 CC departure from the current strategy of treatment prior to formation of
 CC vascular occlusions. The present sequence represents an integrin ligand
 CC dissociator (ILD) that can be used in the method of the invention.

SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 1 EILDV 5

RESULT 5

AAW80488
 ID AAW80488 standard; peptide; 5 AA.

XX AAY0488;
 XX

OS Synthetic.
 PN WO200000477-A1.
 XX
 XX
 PD 06-JAN-2000.
 XX
 XX 31-MAY-1999; 99WO-IB00973.
 XX
 XX 30-JUN-1998; 98US-0091180.
 XX
 XX (PFIZ) PFIZER PROD INC.
 XX
 XX Duplantier AJ, Milici AJ, Chupak LS;
 XX
 XX WPI; 2000-126762/11.
 XX
 XX Arylalkyl and arylureidoalkyl azolyalkanoic acid derivatives -
 XX
 PS Disclosure; Page 2; 120pp; English.
 XX
 XX The invention relates to novel arylalkyl and arylureidoalkyl
 CC azolyalkanoic acid derivatives and related compounds (I), and their
 CC salts and prodrugs. These are are integrin inhibitors, specifically of
 CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
 CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
 CC inducible cell surface protein VCAM-1 (vascular cell adhesion
 CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
 CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,
 CC and consequent or associated pathogenic processes mediated by VLA-4, and
 CC may therefore be useful in the treatment and prevention of inflammatory,
 CC autoimmune, or respiratory disorders. These include asthma, arthritis,
 CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
 CC inflammatory bowel disease. Sequences MAY6918-Y69620 represent peptides
 CC derived from the VLA-4-binding domain of the FN CS-1 region which
 CC contain the LDV motif and are known to inhibit fibronectin-dependent
 CC cell adhesion.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 23; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db |
 |
 |
 |
 1 EILDV 5
 RESULT 8
 AAB73465
 ID AAB73465 standard; peptide; 5 AA.
 XX
 XX AAB73465;
 AC
 XX
 XX 02-JUN-2001 (first entry)
 DT
 XX
 XX Fibronectin VLA-4 binding domain-derived pentapeptide #1.
 DE
 XX Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
 KW very late antigen; antibody; kidney disease; chronic renal failure;
 KW end-stage renal disease; chronic diabetic nephropathy;
 KW diabetic glomerulopathy; diabetic renal hypertrophy;
 KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
 KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
 KW nephrotropic; cell adhesion inhibition; fibronectin CS-1 region.
 XX
 OS Unidentified.
 OS
 XX
 XX WO200119396-A1.
 FN
 XX
 PD 22-MAR-2001.
 PD
 XX 14-SEP-2000; 2000WO-US25140.
 PF

XX 14-SEP-1999; 99US-0153826.
 XX
 XX (BIOJ) BIOGEN INC.
 PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
 XX
 XX Allen A, Pusey C, Lobb R;
 PI
 XX WPI; 2001-273408/28.
 DR
 XX
 XX Treating a mammal in, or at a risk of developing, chronic renal
 PT failure, involves administering at least one integrin antagonist to the
 PT mammal -
 XX
 XX Disclosure; Page 24; 62pp; English.
 PS
 XX The invention relates to a method for treating a mammal with,
 CC or at risk of developing, chronic renal failure, involving the
 CC administration of at least one integrin antagonist. The integrin
 CC antagonists that may be used in the method include antagonists of
 CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
 CC containing integrins. In particular, the antagonists are antibodies
 CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
 CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
 CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
 CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
 CC The method of the invention may be used to treat chronic renal failure,
 CC end-stage renal disease, chronic diabetic nephropathy, diabetic
 CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
 CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
 CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
 CC peptides derived from the VLA-4 binding domain (CS-1 region) of
 CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
 CC therefore be used in the method of the invention.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db |
 |
 |
 |
 1 EILDV 5
 RESULT 9
 AAB91966
 ID AAB91966 standard; Peptide; 5 AA.
 XX
 XX AAB91966;
 AC
 XX
 XX 22-JUN-2001 (first entry)
 DT
 XX
 XX Fibronectin fragment and fibrin related peptide SEQ ID NO:1142.
 DE
 XX
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 XX WO200069900-A2.
 PN
 XX
 XX 23-NOV-2000.
 PD
 XX
 XX 17-MAY-2000; 2000WO-US13576.
 PF
 XX
 XX 17-MAY-1999; 99US-0134406.
 PR
 XX 10-SEP-1999; 99US-0153406.
 PR
 XX 15-OCT-1999; 99US-0159783.
 PR
 XX

PA (CONJ-) CONJUCHEM INC.
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT -
 XX
 XX Disclosure; Page 569; 733pp; English.
 XX
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db |||||
 1 EILDV 5

RESULT 10
 AAB50876
 ID AAB50876 standard; peptide; 5 AA.
 XX
 AC AAB50876;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Integrin recognition peptide sequence #3.
 XX
 KW Integrin; transmembrane protein; alpha4 integrin inhibitor;
 KW paxillin; immunosuppressive; inflammatory bowel disease; arthritis;
 KW multiple sclerosis; asthma; atherosclerosis; wound healing.
 XX
 OS Unidentified.
 XX
 PN WO200073342-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US15153.
 XX
 PR 01-JUN-1999; 99US-0323447.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Ginsberg MH, Pfaff M, Liu S;
 XX WPI; 2001-070959/08.
 XX
 XX Polypeptides useful in construction of structural models for
 PT identifying therapeutic compounds, comprises series of heptad repeats

PT that mimic a transmembrane domain and cytoplasmic domain attached to
 PT heptad repeats -
 XX Disclosure; Page 2; 37pp; English.
 XX
 XX The present sequence is given in a specification relating to a
 CC polypeptide comprising a series of heptad-repeats that mimic a
 CC transmembrane domain, and a selected cytoplasmic domain attached to the
 CC heptad repeats. At least a portion of the polypeptide is prepared
 CC recombinantly or at least 1 heptad repeat in the series has a different
 CC amino acid sequence to other heptad repeats in the series. The
 CC polypeptide is useful in the construction of structural models which are
 CC useful for evaluating structure and activity of a selected occupied and
 CC clustered transmembrane protein having the selected cytoplasmic domain
 CC and for identifying therapeutic compounds. It is also useful for
 CC identifying agents as inhibitors of alpha4 integrin biological
 CC responses by contacting the structural model with paxillin or a
 CC paxillin related molecule in the presence and absence of a test agent
 CC and determining binding of paxillin or paxillin related molecule to the
 CC structural model. A decrease in binding in the presence of the test
 CC agent indicates that the test agent is an inhibitor of alpha4 integrin
 CC biological response. Inhibitors of the binding of paxillin to alpha4 are
 CC useful in blocking immune responses in conditions such as inflammatory
 CC bowel disease, arthritis, multiple sclerosis and asthma and in
 CC inhibiting atherosclerosis and scarring during wound healing.
 XX
 XX Sequence 5 AA;
 SQ

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db |||||
 1 EILDV 5

RESULT 11
 AAB59135
 ID AAB59135 standard; peptide; 5 AA.
 XX
 AC AAB59135;
 XX
 DT 21-MAR-2001 (first entry)
 XX
 DE Peptide #3 recognised by integrin.
 XX
 KW Heptad repeat; transmembrane domain; cytoplasmic; integrin;
 KW inflammation; thrombosis; malignancy.
 XX
 OS Synthetic.
 XX
 PN WO200073341-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14656.
 XX
 PR 27-MAY-1999; 99US-0320907.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Ginsberg MH, Pfaff M;
 XX WPI; 2001-041143/05.
 XX
 XX Polypeptides useful in construction of structural models for
 PT identifying therapeutic compounds, comprises series of heptad repeats
 PT that mimic a transmembrane domain and cytoplasmic domain attached to
 PT the repeats -
 XX Disclosure; Page 2; 36pp; English.
 XX

CC The present invention relates to a peptide with a series of
 CC heptad-repeats that mimic a transmembrane domain and a selected
 CC cytoplasmic domain attached to the heptad repeats. The invention
 CC is useful for evaluating structure and activity of a selected
 CC occupied and clustered transmembrane protein with the selected
 CC cytoplasmic domain and for identifying therapeutic compounds. It
 CC is also useful for identifying a cytoplasmic domain binding partner.
 CC It is may be used to study protein interactions with transmembrane
 CC proteins such as integrin, which can be used to treat conditions in
 CC which over activity of integrins is involved, such as inflammation,
 CC thrombosis and malignancy.

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 12

AAV77443
 ID AAY77443 standard; peptide; 6 AA.

XX AC AAY77443;

XX DT 22-MAY-2000 (first entry)

XX DE Fibronectin CS1-derived peptide #34.

XX KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 XX KM CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 XX KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.

XX OS Mammalia.

XX PN WO200002903-A1.

XX PD 20-JAN-2000.

XX PF 15-DEC-1998; 98WO-US26605.

XX PR 10-JUL-1998; 98US-0113689.

XX PA (CYTE-) CYTEL CORP.

XX PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;

XX DR WPI; 2000-182213/16.

XX PT New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders

XX PS Disclosure; Fig 2; 243pp; English.

XX CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and

CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
 CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAY77410).

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5
 |||||
 Db 2 EILDV 6

RESULT 13

AAV77444
 ID AAY77444 standard; peptide; 6 AA.

XX AC AAY77444;

XX DT 22-MAY-2000 (first entry)

XX DE Fibronectin CS1-derived peptide #35.

XX KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 XX KM CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 XX KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.

XX OS Mammalia.

XX PN WO200002903-A1.

XX PD 20-JAN-2000.

XX PF 15-DEC-1998; 98WO-US26605.

XX PR 10-JUL-1998; 98US-0113689.

XX PA (CYTE-) CYTEL CORP.

XX PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;

XX DR WPI; 2000-182213/16.

XX PT New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders

XX PS Disclosure; Fig 2; 243pp; English.

XX CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either

CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
 CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAY77410).

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 14
 AAW56065
 ID AAW56065 standard; peptide; 7 AA.

XX AC AAW56065;
 XX DT 29-JUL-1998 (first entry)
 XX DE Alpha4 integrins targeting sequence SEQ ID NO:80.

XX KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
 XX KW constrained peptide motif; gene therapy; cancer; heart disease;
 XX KW autoimmune disorder.

XX OS Synthetic.
 XX OS Mastadenovirus.
 XX PN W09807865-A1.

XX PD 26-FEB-1998.

XX PF 21-AUG-1997; 97WO-US14719.

XX PR 21-AUG-1996; 96US-0701124.

XX PA (GENV-) GENVEC INC.

XX PI Kovessdi I, Roelvink PW, Wickham TU;

XX DR WPI; 1998-169169/15.

XX PT Chimeric adenovirus fibre proteins - containing non-native amino
 XX PT acid sequence to provide for binding and entry into cells,
 XX PT especially for gene therapy

XX PS Example 8; Page 57; 124pp; English.

XX CC The present sequence represents an alpha4 integrins targeting sequence,
 XX CC which is used in an example from the present invention. The present
 XX CC invention describes a chimeric adenovirus fibre protein (AFP) containing
 XX CC a constrained non-native amino acid sequence. The non-native amino acid
 XX CC sequence allows the chimeric fibre (or a vector comprising the chimeric
 XX CC fibre) to more efficiently bind to and enter cells. The products can be
 XX CC used for gene therapy, for treating cancer, e.g. melanoma, glioma and
 XX CC lung cancers as well as genetic disorders, e.g. cystic fibrosis,
 XX CC haemophilia and muscular dystrophy as well as pathogenic infections,
 XX CC e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g.
 XX CC prevent restenosis following angioplasty or to promote angiogenesis to
 XX CC reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's
 XX CC disease, colitis, rheumatoid arthritis, and Alzheimer's disease.

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 23; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 15

AAR11361
 ID AAR11361 standard; peptide; 8 AA.

XX AC AAR11361;

XX DT 04-JUN-1991 (first entry)

XX DE Peptide #352 derived from Cs-1 peptide of IIICS region.

XX KW Fibronectin; extracellular matrix receptor; ECMR: type III;
 XX KW connecting segment; IIICS; adhesion; alpha4beta1; lymphocyte;
 XX KW autoimmune disease; allergy; asthma; ligand.

XX OS Synthetic.

XX PN W09103252-A.

XX PD 21-MAR-1991.

XX PF 31-AUG-1990; 90WO-US04978.

XX PR 01-SEP-1989; 89US-0402389.

XX PA (WAYN/) WAYNER E.

XX PI Wayner E;

XX DR WPI; 1991-101865/14.

XX PT Inhibition of lymphocyte adherence to vascular endothelium -
 XX PT using a novel antibody or peptide for treatment of auto-immune
 XX PT disease, asthma, allergy etc.

XX PS Claim 10; Page 74; 92pp; English.

XX CC The peptide is derived the CS-1 peptide (Humphries et al., 1987,
 XX CC J. Biol. Chem. 262:6886-6892), from the IIICS variable region of
 XX CC fibronectin. The peptide inhibits binding of lymphocytes to
 XX CC endothelial cells preventing migration through the vascular
 XX CC endothelium and into tissues. It acts by blocking the alpha4-
 XX CC beta1 extracellular matrix receptor. Admin. of the peptide can
 XX CC suppress the immune response and treat diseases associated with
 XX CC chronic or relapsing activation of the immune system, including
 XX CC collagen vascular diseases and other autoimmune diseases,
 XX CC multiple sclerosis, asthma, allergy and chronic inflammatory skin
 XX CC conditions.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 16

AAR28885
 ID AAR28885 standard; peptide; 8 AA.

XX

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AC AAR28885;
XX
DT 23-MAR-1993 (first entry)
XX
DE Cell adhesion inhibitory peptide.
XX
XX Cell adhesion; cancer; metastasis inhibitor; wound healer;
KW immunosuppressant; platelet; aggregation inhibitor; neuropathy.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "Terminal Glu residue is linked to
XX R1OCH2-CH(OR2)-CH2-OOC-(CH2)m-CO-, where m
XX = 1-5, and R1 and R2 = H or 8-24 opt. substd.,
XX (un)satd. acyl or alkyl; the asymmetric carbon
XX present in the molecule may be facemic or
XX optically active "
XX
XX JP04295497-A.
XX
XX 20-OCT-1992.
XX
XX 26-MAR-1991; 91JP-0062146.
XX
XX 26-MAR-1991; 91JP-0062146.
XX
XX (FUJF ) FUJI PHOTO FILM CO LTD.
XX
XX WPI; 1992-395376/48.
XX
XX Peptide deriv. - useful as cancer metastasis inhibitor, wound
XX healer, immunosuppressant, etc.
XX
XX Claim 1; Page 2; 10pp; Japanese.
XX
XX The sequences given in AAR28885-86 are peptides which have been shown
XX to inhibit cell adhesion. These peptides can be used as the active
XX component in a cancer metastasis inhibitor; a wound healer, an
XX immunosuppressant, a platelet aggregation inhibitor or a neuropathy
XX treating drug.
XX
SQ Sequence 8 AA;
XX
XX Query Match 100.0%; Score 23; DB 13; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 EILDV 5
Db 1 EILDV 5
XX
RESULT 17
AAR44360
ID AAR44360 standard; peptide; 8 AA.
XX
XX AAR44360;
XX
XX 17-APR-1995 (first entry)
XX
XX Polymer-bound cell surface receptor binding peptide.
XX
XX Propenamide; cell adhesion antagonist; anticancer; antitumour;
KW lymphocyte activation; metastasis; cell culture.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "N-terminal is attached to propenamide po"
XX

```

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PN JP06116288-A.
XX
XX 26-APR-1994.
XX
XX 09-OCT-1992; 92JP-0271293.
XX
XX 09-OCT-1992; 92JP-0271293.
XX
XX (FUJF ) FUJI PHOTO FILM CO LTD.
XX
XX WPI; 1994-173758/21.
XX
XX New propenamide cpds. which are N-substd. by specified peptide,
XX and new polymers - are cell adhesion inhibitors useful e.g. for
XX preventing cancer metastasis
XX
XX Claim 1; Page 2; 8pp; Japanese.
XX
XX The invention relates to new propenamide compounds of formula
XX R1R2C=C(R3)CO-(NH)x-A and their (optionally crosslinked) polymers,
XX where R1 and R2 are H or COOH, R3 = H, Me, Et, halo or carboxymethyl,
XX A is a peptide of formula -(R4)x-(CO)x-[(Glu)x-(Ile)x-Leu-Asp-Val-
XX (Pro)x-(Ser)x-(Thr)x]n-(Z)x-(R5)x-; where Z = O or NH, one of R4 and
XX R5 is a terminal H and the other is absent or 1-11C alkylene or 6-
XX 11C arylene each of which may be optionally substituted, n = 1 - 5,
XX and x = 0 or 1. The compounds and their polymers combine with cell
XX surface receptors and prevent cell adhesion. They can be used to
XX inhibit cancer metastasis and to activate lymphocytes, and as
XX components of cell culture substrates.
XX
XX Sequence 8 AA;
XX
XX Query Match 100.0%; Score 23; DB 15; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 EILDV 5
Db 1 EILDV 5
XX
RESULT 18
AAR92536
ID AAR92536 standard; peptide; 8 AA.
XX
XX AAR92536;
XX
XX 09-SEP-1996 (first entry)
XX
XX VLA-4 binding peptide #6.
XX
XX VLA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR;
XX alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis;
XX complementarity determining region; inflammatory brain disorder; therapy;
XX multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis;
XX AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases;
XX rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1
XX /note= "acetylated"
XX
XX WO9601644-A1.
XX
XX 25-JAN-1996.
XX
XX 10-JUL-1995; 95WO-US08516.
XX
XX 06-JUN-1995; 95US-0467580.
XX
XX 11-JUL-1994; 94US-0273055.
XX

```

QY 1 EILDV 5


```

Db      1 EILDV 5
RESULT 21
AAW56046
ID      AAW56046 standard; peptide; 8 AA.
XX
AC      AAW56046;
XX
DT      29-JUL-1998 (first entry)
XX
DE      Chimeric adenovirus fiber protein non-native amino acid sequence 56.
XX
KW      Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW      constrained peptide motif; gene therapy; cancer; heart disease;
KW      autoimmune disorder.
XX
OS      Synthetic.
OS      Mastadenovirus.
XX
PN      WO9807865-A1.
XX
PD      26-FEB-1998.
XX
PF      21-AUG-1997; 97WO-US14719.
XX
PR      21-AUG-1996; 96US-0701124.
XX
PA      (GENV-) GENVEC INC.
XX
PI      Kovessi I, Roelvink PW, Wickham TJ;
XX
WT      WPI; 1998-169169/15.
XX
PT      Chimeric adenovirus fibre proteins - containing non-native amino
PT      acid sequence to provide for binding and entry into cells,
PT      especially for gene therapy
XX
PS      Claim 7; Page 84; 124pp; English.
XX
CC      The present sequence represents a specifically claimed non-native amino
CC      acid sequence from a chimeric adenovirus fibre protein (AFP) of the
CC      present invention. The non-native amino acid sequence allows the
CC      chimeric fibre (or a vector comprising the chimeric fibre) to more
CC      efficiently bind to and enter cells. The products can be used for gene
CC      therapy, for treating cancer, e.g. melanoma, glioma and lung cancers as
CC      well as genetic disorders, e.g. cystic fibrosis, haemophilia and
CC      muscular dystrophy as well as pathogenic infections, e.g. HIV,
CC      tuberculosis and hepatitis and also for heart disease, to e.g. prevent
CC      restenosis following angioplasty or to promote angiogenesis to reperfuse
CC      necrotic tissue, and in autoimmune disorders, e.g. Crohn's disease,
CC      colitis, rheumatoid arthritis, and Alzheimer's disease.
XX
SQ      Sequence 8 AA;

Query Match      100.0%; Score 23; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EILDV 5
Db      1 EILDV 5

RESULT 22
AAW32862
ID      AAW32862 standard; peptide; 8 AA.
XX
AC      AAW32862;
XX
DT      02-NOV-1999 (first entry)
XX
DE      Fibronectin protein IIICS domain peptide.
XX
KW      Fibronectin; extracellular matrix. open wound healing; IIICS domain;
KW      acute gaping cutaneous wound; chronic cutaneous ulcer; therapy;
KW      wound healing promoter; cell binding domain; heparin II binding domain.
XX
OS      Homo sapiens.
XX
PN      WO9942117-A1.
XX
PD      26-AUG-1999.
XX
PF      10-FEB-1999; 99WO-US02872.
XX
PR      18-FEB-1998; 98US-0025622.
XX
DE      Fibronectin protein IIICS domain peptide.

Fibronectin; extracellular matrix; wound healing promoter; IIICS domain;
cell binding domain; heparin II binding domain; haemostasis; therapy;
surgical incisional wound; traumatic wound; radiation wound;
cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.

Homo sapiens.
WO9942126-A1.
26-AUG-1999.
10-FEB-1999; 99WO-US02873.
18-FEB-1998; 98US-0025706.
(UYNY ) UNIV NEW YORK STATE RES FOUND.
Clark RA, Gallit J, Greiling D;
WPI; 1999-527421/44.
Extracellular matrix for promoting wound healing containing
recombinant fibronectin-derived peptide and backbone matrix
Claim 6; Page 21; 48pp; English.
This sequence represents a fibronectin protein fragment used in the
extracellular matrix (A) of the invention. (A) is used for promoting
wound healing, and comprises a recombinant fibronectin peptide,
containing peptide fragments from at least two fibronectin domains, and a
backbone matrix. The fibronectin domain peptides used are preferably from
the IIICS domain, the cell binding domain, or the heparin II binding
domain of human fibronectin. (A) provides haemostasis and an environment
that recruits new tissue cells to the site of the wound. (A) is used to
promote healing of acute or chronic wounds, e.g. surgical incisional
wounds, traumatic wounds, radiation wounds, cancer extirpations, venous
leg ulcers, diabetic ulcers and pressure ulcers.

Query Match      100.0%; Score 23; DB 20; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EILDV 5
Db      1 EILDV 5

RESULT 23
AAW32874
ID      AAW32874 standard; peptide; 8 AA.
XX
AC      AAW32874;
XX
DT      02-NOV-1999 (first entry)
XX
DE      Fibronectin protein IIICS domain peptide.
XX
KW      Fibronectin; extracellular matrix. open wound healing; IIICS domain;
KW      acute gaping cutaneous wound; chronic cutaneous ulcer; therapy;
KW      wound healing promoter; cell binding domain; heparin II binding domain.
XX
OS      Homo sapiens.
XX
PN      WO9942117-A1.
XX
PD      26-AUG-1999.
XX
PF      10-FEB-1999; 99WO-US02872.
XX
PR      18-FEB-1998; 98US-0025622.
XX
DE      Fibronectin protein IIICS domain peptide.

```

XX (UYNV) UNIV NEW YORK STATE RES FOUND.
 PA Clark RA, Grelling D;
 PI WPI; 1999-527415/44.
 XX
 DR New extracellular matrix used to accelerate healing of acute gaping
 PT cutaneous wounds and chronic cutaneous ulcers
 PT
 XX Claim 5; Page 19; 43pp; English.
 XX
 CC This sequence represents a fibronectin protein fragment used in the
 CC extracellular matrix of the invention. The extracellular matrix comprises
 CC two or more fibronectin domains in a backbone matrix, and is used to
 CC enhance wound healing. The fibronectin domain peptides used are
 CC preferably from the IIRCS domain, the cell binding domain, or the
 CC heparin II binding domain of human fibronectin. The matrix facilitates
 CC wound healing by providing an environment that intrinsically recruits new
 CC tissue cells to the wound site. The new matrix is useful for facilitating
 CC wound healing, especially useful for treating open wounds such as acute
 CC gaping cutaneous wounds and chronic cutaneous ulcers. The problem of
 CC chronic, non-healing wounds is severe. These open wounds require
 CC long-term care and procedures that are costly and labour intensive.
 CC Furthermore, these wounds have a severe impact on the patients' quality of
 CC life. Prior compositions and matrices have not been useful or cost
 CC effective. The present invention provides a matrix for wound healing
 CC that meets these requirements, and overcomes the deficiencies of the
 CC prior matrices.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 23; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 DB 1 EILDV 5
 RESULT 24
 AAB35734
 ID AAB35734 standard; peptide; 8 AA.
 XX
 AC AAB35734;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Vitronectin peptide used to enhance viral vector binding affinity.
 XX
 KW Pharmaceutical composition; gene therapy; junctional complex disruption;
 KW cystostatic; cardiant; vasotropic; antiinflammatory; antilipaeamic;
 KW cystic fibrosis; inflammatory disease; fibrotic lung disease;
 KW peripheral vascular disease; coronary arterial disease; restenosis;
 KW hypercholesterolaemia; cancer; human; vitronectin.
 XX
 OS Unidentified.
 XX
 XX WO200062815-A2.
 XX
 XX 26-OCT-2000.
 XX
 XX 13-APR-2000; 2000WO-GB01408.
 XX
 PR 15-APR-1999; 99GB-0008636.
 PR 15-APR-1999; 99GB-0008643.
 PR 20-APR-1999; 99GB-0009073.
 PR 22-APR-1999; 99GB-0009297.
 PR 13-SEP-1999; 99US-0153757.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 (UYNV-) UNIV NORTH CAROLINA.
 Boucher RC, Ford MJ, Johnson LG, Man Y, West MR;
 WPI; 2000-679557/66.
 Novel pharmaceutical composition useful for gene therapy, comprises
 nucleic acid encoding therapeutic gene and a promoter, transfection
 vehicle and an agent which disrupts function of junctional complex in
 cells -
 Disclosure; Page 12; 51pp; English.
 This invention relates to a pharmaceutical composition used for gene
 therapy, comprising a nucleic acid encoding a therapeutic gene and a
 promoter, a transfection vehicle and an agent to disrupt the function of
 the junctional complex in the cells. The pharmaceutical composition has
 cytostatic, cardiant, vasotropic, antiinflammatory and antilipaeamic
 activity. The pharmaceutical composition is useful for gene therapy and
 for enhancing efficiency of gene delivery to cells. The composition is
 useful for gene therapy of cystic fibrosis, inflammatory or fibrotic lung
 diseases, peripheral vascular disease, coronary arterial diseases,
 restenosis, hypercholesterolaemia and cancer. The present sequence
 represents a vitronectin peptide. The peptide can be used to enhance the
 binding affinity of a viral vector used in the pharmaceutical
 composition of the invention.
 Sequence 8 AA;
 Query Match 100.0%; Score 23; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 DB 1 EILDV 5
 RESULT 25
 AAY80489
 ID AAY80489 standard; peptide; 8 AA.
 XX
 AC AAY80489;
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Cell adhesion peptide #24.
 XX
 KW Bone regenerative; osteopathic; osseous tissue; reconstitution;
 KW scaffold matrix; bone formation promoter; bone resorption inhibitor;
 KW cell adhesion; osteoblast; osteoclast; bone defect; fracture.
 XX
 OS Synthetic.
 XX
 PN WO200004941-A1.
 XX
 PD 03-FEB-2000.
 XX
 XX 22-JUL-1999; 99WO-US16800.
 XX
 PR 24-JUL-1998; 98US-0122348.
 XX
 XX (PHAR-) PHARMACAL BIOTECHNOLOGIES INC.
 PA Budny JA;
 PI WPI; 2000-195084/17.
 DR
 XX System for reconstructing osseous tissue, useful e.g. for treating
 PT fractures, comprises scaffold containing promoter of bone formation and
 PT inhibitor of bone resorption -
 XX
 XX Claim 14; Page 32; 44pp; English.

XX The invention relates to a novel system for reconstitution of osseous
 CC tissue comprising a scaffold carrying a compound (I) that promotes
 CC bone formation and a component that decreases bone resorption (II).
 CC (I) induces migration and adhesion of osteoblasts and osteoclasts and
 CC (II) inhibits proteolysis (specifically by plasmin) of extracellular
 CC matrix. (I) is preferably selected from: selectin or selectin binding
 CC fragments, proteins and peptides that facilitate cell adhesion,
 CC plasminogen activator inhibitors. The peptides AAY80466-Y80492 are claimed
 CC metalloprotease inhibitors. The peptides AAY80466-Y80492 are claimed
 CC examples of cell adhesion peptides used in the system of the invention.
 CC The system is used to replace, remodel or correct bone defects, e.g.
 CC fractures, fissures or bone mass loss. Incorporation of (I) into the
 CC scaffold results in rapid seeding by osteoblasts and the development of
 CC an organic matrix, i.e. the preformed scaffold replaces the
 CC rate-determining step of extracellular matrix formation. The scaffold can
 CC be designed to have a predetermined resorption/degradation rate, and may
 CC include regulatory compounds for specific cell types.

XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 23; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 26
 AAY69618
 ID AAY69618 standard; peptide; 8 AA.
 XX
 AC AAY69618;
 XX
 DT 19-APR-2000 (first entry)
 DE
 DE VLA-4 inhibitor peptide #1.
 XX
 XX LDV peptide: VLA-4 inhibitor; very late antigen; alpha-4-beta-1;
 KW CD49d/CD29; cell adhesion; arylalkyl azolylalkanoic acid derivative;
 KW arylureidoalkyl azolylalkanoic acid derivative; inflammatory disorder;
 KW autoimmune disorder; respiratory disorder; LDV motif.
 XX
 XX Synthetic.
 OS
 XX WO200000477-A1.
 PN
 PD 06-JAN-2000.
 XX
 XX 31-MAY-1999; 99WO-IB00973.
 PF
 PF 30-JUN-1998; 98US-0091180.
 PR
 XX (PFIZ) PFIZER PROD INC.
 PA
 PA Duplantier AJ, Milici AJ, Chupek LS;
 PI
 XX WPI; 2000-126762/11.
 DR
 XX Arylalkyl and arylureidoalkyl azolylalkanoic acid derivatives -
 XX
 XX Disclosure; Page 2; 120pp; English.

XX The invention relates to novel arylalkyl and arylureidoalkyl
 CC azolylalkanoic acid derivatives and related compounds (I), and their
 CC salts and prodrugs. These are are integrin inhibitors, specifically of
 CC VLA-4 (very late antigen 4, also known as alpha-4-beta-1 or CD49d/CD29),
 CC which mediate cell adhesion. VLA-4 is a receptor for the cytokine-
 CC inducible cell surface protein VCAM-1 (vascular cell adhesion
 CC molecule-1) and for the alternatively spliced forms of fibronectin (FN)
 CC which contain the CS-1 domain. The novel compounds inhibit cell adhesion,

CC and consequent or associated pathogenic processes mediated by VLA-4, and
 CC may therefore be useful in the treatment and prevention of inflammatory,
 CC autoimmune, or respiratory disorders. These include asthma, arthritis,
 CC psoriasis, multiple sclerosis, transplant rejection, diabetes, and
 CC inflammatory bowel disease. Sequences AAY69618-Y69620 represent peptides
 CC derived from the VLA-4-binding domain of the FN CS-1 region which
 CC contain the LDV motif and are known to inhibit fibronectin-dependent
 CC cell adhesion.

XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 23; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 27
 AAB73464
 ID AAB73464 standard; peptide; 8 AA.
 XX
 AC AAB73464;
 XX
 DT 02-JUL-2001 (first entry)
 DE
 DE Fibronectin VLA-4 binding domain-derived octapeptide.
 XX
 XX Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
 KW very late antigen; antibody; kidney disease; chronic renal failure;
 KW end-stage renal disease; chronic diabetic nephropathy;
 KW diabetic glomerulopathy; diabetic renal hypertrophy;
 KW hypertensive nephrosclerosis; hypertensive glomerulosclerosis;
 KW chronic glomerulonephritis; hereditary nephritis; renal dysplasia;
 KW nephrotic; cell adhesion inhibition; fibronectin CS-1 region.
 XX
 OS Unidentified.
 XX
 XX WO200119396-A1.
 PN
 XX 22-MAR-2001.
 PD
 XX 14-SEP-2000; 2000WO-US25140.
 PF
 XX 14-SEP-1999; 99US-0153826.
 PR
 XX (BIOJ) BIOGEN INC.
 PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
 PA
 XX Allen A, Pusey C, Lobb R;
 PI
 XX WPI; 2001-273408/28.
 DR
 XX Treating a mammal in, or at a risk of developing, chronic renal
 PT failure, involves administering at least one integrin antagonist to the
 PT mammal -
 PT
 XX Disclosure; Page 24; 62pp; English.

XX The invention relates to a method for treating a mammal with,
 CC or at risk of developing, chronic renal failure, involving the
 CC administration of at least one integrin antagonist. The integrin
 CC antagonists that may be used in the method include antagonists of
 CC alpha-4-subunit containing integrins or antagonists of alpha-1-subunit-
 CC containing integrins. In particular, the antagonists are antibodies
 CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
 CC VLA-4 (alpha-4-beta-1 integrin) which inhibit the interaction of the
 CC integrin and its cognate ligand (collagen I, collagen IV, and laminin in
 CC the case of VLA-1, and fibronectin and VCAM-1 in the case of VLA-4).
 CC The method of the invention may be used to treat chronic renal failure,
 CC end-stage renal disease, chronic diabetic nephropathy, diabetic

CC glomerulopathy, diabetic renal hypertrophy, hypertensive nephrosclerosis,
 CC hypertensive glomerulosclerosis, chronic glomerulonephritis, hereditary
 CC nephritis or renal dysplasia. Sequences AAB73464-AAB73466 represent
 CC peptides derived from the VLA-4 binding domain (CS-1 region) of
 CC fibronectin, which inhibit fibronectin-dependent cell adhesion, and may
 CC therefore be used in the method of the invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 28

AAB91967
 ID AAB91967 standard; Peptide; 8 AA.

XX AC AAB91967;

XX DT 22-JUN-2001 (first entry)

XX DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1143.

XX KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX OS Synthetic.

XX FN WO200069900-A2.

XX PD 23-NOV-2000.

XX PF 17-MAY-2000; 2000WO-US13576.

XX PR 17-MAY-1999; 99US-0134406.

XX PR 10-SEP-1999; 99US-0153406.

XX PR 15-OCT-1999; 99US-0159783.

XX PA (CONJ-) CONJUCHEM INC.

XX PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX DR WPI; 2001-112059/12.

XX PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

XX PS Disclosure; Page 569; 733pp; English.

XX CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 29

AAR29631
 ID AAR29631 standard; peptide; 9 AA.

XX AC AAR29631;

XX DT 26-JAN-1993 (first entry)

XX DE Adhesion inhibitor peptide #1.

XX KW Triazine; polyethylene glycol; agglutination.

XX OS Synthetic.

XX PN JP04187698-A.

XX PD 06-JUL-1992.

XX PF 21-NOV-1990; 90JP-0316441.

XX PR 21-NOV-1990; 90JP-0316441.

XX PA (FUJIF) FUJIFILM CO LTD.

XX DR WPI; 1992-274053/33.

XX PT New peptide(s) contg. PEG derivs. - are cell adhesion and
 PT platelet adhesion inhibitors, useful as carcinoma metastasis
 PT inhibitors, immuno-regulators and for wound healing

XX PS Disclosure; Page 3; 11pp; Japanese.

XX CC One of 1 or 2 of these chains are attached via the N- or C-terminal to
 CC a 2,4,6-trisubstituted s-triazine ring, where one substitution is a
 CC polyethylene glycol chain [CH₃(OCH₂CH₂)_n-O- (n= 1-150)] and the
 CC other is either another, same, polyethylene glycol chain, or another,
 CC same, peptide chain. These PEG derivatives or their salts are useful as
 CC animal cell adhesion inhibitors, or as platelet agglutination or
 CC adhesion inhibitors. They may also be used as carcinoma metastasis
 CC inhibitors, wound healing drugs and immunoregulators.

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 2 EILDV 6

RESULT 30

AAR30433
 ID AAR30433 standard; peptide; 9 AA.

XX AC AAR30433;

XX DT 04-FEB-1993 (first entry)

XX

DE Cell adhesion inhibitor #2.
 KW platelet aggregation inhibitor; platelet adhesion inhibitor;
 KW fibronectin.
 XX Synthetic.
 OS
 PN JP04198194-A.
 XX
 XX 17-JUL-1992.
 XX
 XX 28-NOV-1990; 90JP-0326224.
 PF
 XX 28-NOV-1990; 90JP-0326224.
 PR
 XX (FUJF) FUJI PHOTO FILM CO LTD.
 PA
 XX WPI; 1992-288936/35.
 DR
 XX New polypeptide(s) contg. repeat units of octa:peptide(s) - for
 PT inhibiting adhesion of cells (e.g. to fibronectin) and
 PT aggregation adhesion of platelets
 XX
 PS Disclosure; Page 1; 8pp; Japanese.
 XX
 CC This sequence represents an animal cell adhesion peptide. It is
 CC useful as an animal cell adhesion inhibitor or platelet aggregation/
 CC adhesion inhibitor.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 23; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 2 EILDV 6

RESULT 31
 AAR28886
 ID AAR28886 standard; peptide; 9 AA.
 XX
 AC AAR28886;
 XX
 DT 23-MAR-1993 (first entry)
 XX
 AC AAR28886;
 XX
 DT 23-MAR-1993 (first entry)
 XX
 DE Cell adhesion inhibitory peptide #2.
 XX
 KW Cell adhesion; cancer; metastasis inhibitor; wound healer;
 KW immunosuppressant; platelet; aggregation inhibitor; neuropathy.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Terminal Gly residue is linked to
 FT R1OCH2-CH(OR2)-CH2-OOC-(CH2)m-CO-, where m
 FT = 1-5, and R1 and R2 = H or 8-24 opt. substnd.,
 FT (un)satd. acyl or alkyl; the asymmetric carbon
 FT present in the molecule may be racemic or
 FT optically active "
 XX
 PN JP04295497-A.
 XX
 XX 20-OCT-1992.
 PD
 XX 26-MAR-1991; 91JP-0062146.
 PF
 XX 26-MAR-1991; 91JP-0062146.
 PR
 XX (FUJF) FUJI PHOTO FILM CO LTD.
 PA

XX WPI; 1992-395376/48.
 DR
 XX Peptide deriv. - useful as cancer metastasis inhibitor, wound
 PT healer, immunosuppressant, etc.
 XX
 XX Claim 1; Page 2; 10pp; Japanese.
 PS
 XX The sequences given in AAR28885-86 are peptides which have been shown
 CC to inhibit cell adhesion. These peptides can be used as the active
 CC component in a cancer metastasis inhibitor, a wound healer, an
 CC immunosuppressant, a platelet aggregation inhibitor or a neuropathy
 CC treating drug.
 XX
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 23; DB 13; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EILDV 5
 Db 2 EILDV 6

RESULT 32
 AAY77436
 ID AAY77436 standard; peptide; 9 AA.
 XX
 AC AAY77436;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fibronectin CS1-derived peptide #27.
 XX
 KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
 XX
 OS Mammalia.
 XX
 PN WO200002903-A1.
 XX
 PD 20-JAN-2000.
 XX
 PF 15-DEC-1998; 98WO-US26605.
 XX
 PR 10-JUL-1998; 98US-0113689.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 XX Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
 PI
 XX WPI; 2000-182213/16.
 DR

New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders
 XX
 PS Disclosure; Fig 1; 243pp; English.
 XX

The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system

CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
 CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAY77410).

XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 23; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 1 EILDV 5

RESULT 33
 AAY77437
 ID AAY77437 standard; peptide; 9 AA.

XX AC AAY77437;

XX DT 22-MAY-2000 (first entry)

XX DE Fibronectin CS1-derived peptide #28.

XX KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.

XX OS Mammalia.

XX FN WO200002903-A1.

XX PD 20-JAN-2000.

XX PF 15-DEC-1998; 98WO-US26605.

XX PR 10-JUL-1998; 98US-0113689.

XX PA (CYTE-) CYTEL CORP.

XX PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;

XX DR WPI; 2000-182213/16.

XX PT New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders -

XX PS Disclosure; Fig 1; 243pp; English.

XX CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,

CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
 CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAY77410).

XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 23; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 |||||
 Db 3 EILDV 7

RESULT 34

AAY77438
 ID AAY77438 standard; peptide; 9 AA.

XX AC AAY77438;

XX DT 22-MAY-2000 (first entry)

XX DE Fibronectin CS1-derived peptide #29.

XX KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.

XX OS Mammalia.

XX FN WO200002903-A1.

XX PD 20-JAN-2000.

XX PF 15-DEC-1998; 98WO-US26605.

XX PR 10-JUL-1998; 98US-0113689.

XX PA (CYTE-) CYTEL CORP.

XX PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;

XX DR WPI; 2000-182213/16.

XX PT New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders -

XX PS Disclosure; Fig 1; 243pp; English.

XX CC The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and

CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
 CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAY77410).

XX
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 4 EILDV 8
 |||||

RESULT 35
 AAY77439
 ID AAY77439 standard; peptide; 9 AA.
 XX AC
 AC AAY77439;
 XX 22-MAY-2000 (first entry)
 DT
 DE Fibronectin CS1-derived peptide #30.
 XX
 XX Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
 XX
 OS Mammalia.

PN WO200002903-A1.
 XX 20-JAN-2000.
 PD
 PF 15-DEC-1998; 98WO-US26605.
 XX
 PR 10-JUL-1998; 98US-0113689.
 XX
 PA (CYTE-) CYTEL CORP.
 XX
 PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
 XX WPI; 2000-182213/16.
 XX
 XX New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders
 XX
 PS Disclosure; Fig 1; 243pp; English.

XX
 XX The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory
 CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either

CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAY77411-Y77414
 CC and AAY77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAY77410).

XX
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 5 EILDV 9
 |||||

RESULT 36
 AAR25998
 ID AAR25998 standard; peptide; 10 AA.
 XX AC
 AC AAR25998;
 XX 26-JAN-1993 (first entry)
 DT
 DE Adhesion inhibitor peptide.
 XX
 XX Triazine; polyethylene glycol; agglutination.
 KW
 XX Synthetic.
 OS
 PH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Any amino acid, or may be absent"
 FT Misc-difference 10 /note= "Any amino acid, or may be absent"
 FT
 XX JP04187698-A.
 XX 06-JUL-1992.
 PD
 PF 21-NOV-1990; 90JP-0316441.
 XX
 PR 21-NOV-1990; 90JP-0316441.
 XX
 PA (FUJF) FUJII PHOTO FILM CO LTD.
 XX WPI; 1992-274053/33.
 DR
 XX New peptide(s) contg. PEG derivs. - are cell adhesion and
 PT platelet adhesion inhibitors, useful as carcinoma metastasis
 PT inhibitors, immuno-regulators and for wound healing
 XX
 PS Claim 1 and 2; Page 1; 11pp; Japanese.

XX
 CC One of 1 or 2 of these chains are attached via the N- or C-terminal to
 CC a 2,4,6-trisubstituted s-triazine ring, where one substitution is a
 CC polyethylene glycol chain [CH₃(OCH₂CH₂)_n-O- (n= 1-150)] and the
 CC other is either another, same, polyethylene glycol chain, or another,
 CC same, peptide chain. For examples see also AAR29631-32. These PEG
 CC derivatives or their salts are useful as animal cell adhesion inhibitors,
 CC or as platelet agglutination or adhesion inhibitors. They may also be
 CC used as carcinoma metastasis inhibitors, wound healing drugs and
 CC immunoregulators.

XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db |||||
 2 EILDV 6

RESULT 37

AAR30432
 ID AAR30432 standard; peptide; 10 AA.

XX AC AAR30432;
 XX DT 04-FEB-1993 (first entry)
 XX DE Cell adhesion inhibitor #1.
 XX DE platelet aggregation inhibitor; platelet adhesion inhibitor;
 XX KW fibronectin.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1
 FT Misc-difference 10 /note= "May be an amino acid, peptide or absent."
 FT Misc-difference 10 /note= "May be an amino acid, peptide or absent."
 XX XX JP04198194-A.
 XX PN 17-JUL-1992.
 XX PD 28-NOV-1990; 90JP-0326224.
 XX PF 28-NOV-1990; 90JP-0326224.
 XX PR (FUJF) FUJI PHOTO FILM CO LTD.
 XX PA WPI; 1992-288936/35.
 XX DR New polypeptide(s) contg. repeat units of octa:peptide(s) - for
 XX PT inhibiting adhesion of cells (e.g. to fibronectin) and
 XX PT aggregation adhesion of platelets
 XX PS Claim 1; Page 1; 8pp; Japanese.
 XX CC This sequence represents an animal cell adhesion peptide. It may be
 CC a repeating unit of up to 10 times the sequence given. It is useful
 CC as an animal cell adhesion inhibitor or platelet aggregation/
 CC adhesion inhibitor.
 XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db |||||
 2 EILDV 6

RESULT 38

AAR29103
 ID AAR29103 standard; peptide; 10 AA.

XX AC AAR29103;
 XX DT 05-APR-1993 (first entry)
 XX DE Platelet aggregation inhibitor #1.
 XX KW platelet aggregation; cell adhesion; cancer metastasis inhibitor;

KW wound healing; immune inhibitor; neuropathy drug.
 XX Synthetic.
 XX OS Key Location/Qualifiers
 FH Misc-difference 1 /note= "Any amino acid or absent
 FT may also have opt -CO- followed by an opt.
 FT substd. (un) satd. 8-24 C alkyl."
 FT Misc-difference 10 /note= "Any amino acid or absent
 FT may also have opt. -O- or -NH- followed by
 FT an opt substd. (un) satd. 8-24 C alkyl."
 XX XX JP04297495-A.
 XX PN 21-OCT-1992.
 XX PD 26-MAR-1991; 91JP-0062148.
 XX PF 26-MAR-1991; 91JP-0062148.
 XX PR (FUJF) FUJI PHOTO FILM CO LTD.
 XX PA WPI; 1992-401809/49.
 XX DR Peptide deriv., for cancer metastasis inhibitor - useful as wound
 XX PT healer, immune- and platelet aggregation inhibitor and neuropathy
 XX PT treating drug
 XX PS Claim 1; Page 1; 9pp; Japanese.
 XX CC This peptide deriv. inhibits adhesion of animal cells, partic
 CC platelet aggregation. The deriv. can be used in cancer metastasis
 CC inhibitors, wound healers, immune inhibitors, platelet aggregation
 CC inhibitors or drugs for treating neuropathy.
 XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db |||||
 2 EILDV 6

RESULT 39

AAR29105
 ID AAR29105 standard; peptide; 10 AA.

XX AC AAR29105;
 XX DT 05-APR-1993 (first entry)
 XX DE Platelet aggregation inhibitor #2.
 XX KW platelet aggregation; cell adhesion; cancer metastasis inhibitor;
 XX KW wound healing; immune inhibitor; neuropathy drug.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 10 /note= "has -O-R where R may be C16H33, C20H41, or
 FT CH2CH2CH(CH3)(CH2)3CH(CH3)(CH2)3-
 FT -CH(CH3)(CH2)3CH(CH3)2"
 XX PN JP04297495-A.
 XX PD 21-OCT-1992.
 XX XX

PF 26-MAR-1991; 91JP-0062148.
PR 26-MAR-1991; 91JP-0062148.
XX (FUJF) FUJI PHOTO FILM CO LTD.
XX WPI; 1992-401809/49.
XX Peptide deriv., for cancer metastasis inhibitor - useful as wound
PT healer, immune- and platelet aggregation inhibitor and neuropathy
PT treating drug
XX Disclosure; Page 3; 9pp; Japanese.
XX This peptide deriv. inhibits adhesion of animal cells, partic
CC platelet aggregation. The deriv. can be used in cancer metastasis
CC inhibitors, wound healers, immune inhibitors, platelet aggregation
CC inhibitors or drugs for treating neuropathy.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 2 EILDV 6
RESULT 40
AAR29106
ID AAR29106 standard; peptide; 10 AA.
XX
AC AAR29106;
XX
DT 05-APR-1993 (first entry)
XX
DE Platelet aggregation inhibitor #3.
XX
KW platelet aggregation; cell adhesion; cancer metastasis inhibitor;
KW wound healing; immune inhibitor; neuropathy drug.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 10 /note= "has -NH-C18H37, or -NH-C14H29."
FT
XX JP04297495-A.
XX 21-OCT-1992.
XX
XX 26-MAR-1991; 91JP-0062148.
XX
XX (FUJF) FUJI PHOTO FILM CO LTD.
XX WPI; 1992-401809/49.
XX Peptide deriv., for cancer metastasis inhibitor - useful as wound
PT healer, immune- and platelet aggregation inhibitor and neuropathy
PT treating drug
XX Disclosure; Page 3; 9pp; Japanese.
XX This peptide deriv. inhibits adhesion of animal cells, partic
CC platelet aggregation. The deriv. can be used in cancer metastasis
CC inhibitors, wound healers, immune inhibitors, platelet aggregation
CC inhibitors or drugs for treating neuropathy.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 2 EILDV 6
RESULT 41
AAR29107
ID AAR29107 standard; peptide; 10 AA.
XX
AC AAR29107;
XX
DT 05-APR-1993 (first entry)
XX
DE Platelet aggregation inhibitor #4.
XX
KW platelet aggregation; cell adhesion; cancer metastasis inhibitor;
KW wound healing; immune inhibitor; neuropathy drug.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "has C16H33, C14H29"
FT
XX JP04297495-A.
XX 21-OCT-1992.
XX
XX 26-MAR-1991; 91JP-0062148.
XX
XX 26-MAR-1991; 91JP-0062148.
XX (FUJF) FUJI PHOTO FILM CO LTD.
XX WPI; 1992-401809/49.
XX Peptide deriv., for cancer metastasis inhibitor - useful as wound
PT healer, immune- and platelet aggregation inhibitor and neuropathy
PT treating drug
XX Disclosure; Page 3; 9pp; Japanese.
XX This peptide deriv. inhibits adhesion of animal cells, partic
CC platelet aggregation. The deriv. can be used in cancer metastasis
CC inhibitors, wound healers, immune inhibitors, platelet aggregation
CC inhibitors or drugs for treating neuropathy.
XX
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 2 EILDV 6
RESULT 42
AAR29108
ID AAR29108 standard; peptide; 10 AA.
XX
AC AAR29108;
XX
DT 05-APR-1993 (first entry)
XX
DE Platelet aggregation inhibitor #5.
XX

CC specific VLA-4 recognition of CS-1 has been identified as the tripeptide
 CC LDV. The generic peptidomimetic inhibits the binding of Jurkat cells
 CC (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay
 CC in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to
 CC or upto about 3000-fold greater than the inhibition in the binding
 CC exhibited by the present standard peptide sequence. CS-1 mediated
 CC inflammation, e.g. asthma, rheumatoid arthritis, osteoarthritis,
 CC allograft rejection, skin inflammation or central nervous system
 CC demyelinating disease, can be treated by the peptidomimetics. See
 CC AAW01706-27 for exemplary inhibitor peptides.

XX
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 3 EILDV 7
 |||||

RESULT 45

AAW01725
 ID AAW01725 standard; peptide; 10 AA.
 AC AAW01725;
 XX
 XX
 DT 16-APR-1997 (first entry)
 DE Inhibitor of fibronectin CS-1 peptide and VLA-4 receptor binding.
 XX
 XX fibronectin; high affinity; CS-1; recognition sequence; VLA-4;
 KW alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor;
 KW leukocyte trafficking function; peptidomimetic; treatment; asthma;
 KW rheumatoid arthritis; osteoarthritis; allograft rejection;
 KW skin inflammation; central nervous system demyelinating disease.
 XX
 OS Synthetic.

XX
 XX WO9515973-A1.
 PN
 XX
 XX 15-JUN-1995.
 PD
 XX
 XX 05-DEC-1994; 94WO-US13943.
 XX
 XX 02-DEC-1994; 94US-0164101.
 PR
 PR 06-DEC-1993; 93US-0164101.
 XX
 XX (CYTE-) CYTEL CORP.
 PA
 XX
 XX Arrhenius TS, Elices MJ, Gaeta FCA;
 PI
 XX
 XX WPI; 1995-224284/29.
 DR
 XX
 XX New peptide mimics of fibronectin CS-1 sequence - inhibit
 FT interaction of endothelial cells and VLA-4, carrying inflammatory
 PT cells, for treating or preventing asthma, arthritis etc.
 XX
 XX Disclosure; Page 36; 103pp; English.

XX
 XX The alpha-4 beta-1 (CD49d/CD29, VLA-4) cell adhesion receptor is an
 CC active participant in leukocyte trafficking functions. Binding of
 CC inflammatory cells to endothelial cells that express the CS-1 portion
 CC (AAW01703) of fibronectin on their surfaces can be inhibited by CS-1
 CC peptidomimetic cpds. of minimal length. A minimal essential sequence for
 CC specific VLA-4 recognition of CS-1 has been identified as the tripeptide
 CC LDV. A generic peptidomimetic inhibits the binding of Jurkat cells
 CC (ATCC TIB 152) to a solid phase-bound CS-1 peptide in an in vitro assay
 CC in an aq. buffer at a pH value of 7.2-7.4 to an extent that is equal to
 CC or upto about 3000-fold greater than the inhibition in the binding
 CC exhibited by AAW01705. CS-1 mediated inflammation, e.g. asthma,
 CC rheumatoid arthritis, osteoarthritis, allograft rejection, skin

CC inflammation or central nervous system demyelinating disease, can be
 CC treated by the peptidomimetics. AAW01706-27 are exemplary inhibitor
 CC peptides.

XX
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 3 EILDV 7
 |||||

RESULT 46

AAW95804
 ID AAR95804 standard; peptide; 10 AA.
 XX
 AC AAR95804;
 XX
 XX
 DT 04-DEC-1996 (first entry)
 DE Alpha-4Beta-1 integrin binding inhibitory peptide 101.
 XX
 XX VCAW-1; vascular cell adhesion molecule-1; VLA-4; very late antigen-4;
 KW inhibitor; binding; white blood cell; migration; capillary wall;
 KW tissue damage; injury; fibronectin; extracellular matrix glycoprotein;
 KW CS1; CS5; HI; LDV; active site.
 KW
 XX
 OS Synthetic.

XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 10
 FT /note= "Thr-NH2"
 XX
 XX US5510332-A.
 PN
 XX
 XX 23-APR-1996.
 PD
 XX
 XX 07-JUL-1994; 94US-0271830.
 PF
 XX
 XX 07-JUL-1994; 94US-0271830.
 PR
 XX
 XX (TEXA-) TEXAS BIOTECHNOLOGY CORP.
 PA
 XX
 XX Beck PJ, Kogan TP, Ren K, Vanderslice P;
 PI
 XX
 XX WPI; 1996-221274/22.
 DR
 XX
 XX New peptide(s) based on the LDV domain of fibronectin - used for
 PT inhibiting binding of alpha-4, beta-1 integrin to VCAW-1,
 PT fibronectin or invasin
 PT
 XX
 XX Disclosure; Column 67-68; 35pp; English.

XX
 XX Vascular cell adhesion molecule-1 (VCAW-1) is protein found on the
 CC surface of endothelial cells that line the interior wall of capillaries.
 CC VCAW-1 recognises and binds to the integrin alpha-4beta-1 (IA4B1; or
 CC VLA-4 for very late antigen-4), a heterodimeric protein present on the
 CC surface of certain white blood cells. Binding of IA4B1 to VCAW-1 allows
 CC white blood cells to adhere to the capillary wall in areas where the
 CC tissue surrounding the capillary has been infected or damaged. Sometimes
 CC this white blood cell migration can become uncontrolled, with white
 CC blood cells flooding to the scene, causing widespread tissue damage.
 CC Cpds. capable of blocking this process may be beneficial as therapeutic
 CC agents. IA4B1 also recognises the extracellular matrix glycoprotein
 CC fibronectin. Three distinct IA4B1-binding sites have been identified
 CC within fibronectin. One site is found in the HeplI region and is
 CC expressed in all isoforms; two others (CS1 and CS5) are present in the
 CC alternatively spliced type III connecting segments. CS1 has the higher
 CC affinity for IA4B1 and contains the tripeptide LDV as its minimal active
 CC site. Peptides AAR95704-805 are modeled after a portion of the CS1

CC peptide that include the LDV domain presented in such a way by its novel
 CC flanking sequence to produce a potent inhibitor of IAB1 binding.

SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 17; Length 10;

Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 3 EILDV 7

RESULT 47

AAW70543
 ID AAW70543 standard; peptide; 10 AA.

XX

XX

XX AAW70543;

DT 26-JAN-1999 (first entry)

XX CS-1 peptide fragment 1 (a fibronectin fragment).

DE Integrin; alpha-4 chain; immunoglobulin; chimeric; heterodimer complex;
 KW inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
 KW CS-1; fibronectin.

XX Synthetic.

OS WO9832771-A1.

PN 30-JUL-1998.

XX

XX 29-JAN-1998; 98WO-JP00370.

XX 29-AUG-1997; 97JP-0234544.

PR 29-JAN-1997; 97JP-0015118.

XX (TORA) TORAY IND INC.

XX Kainoh M, Tanaka T;

XX WPI; 1998-427881/36.

XX

XX

XX

XX Integrin-immunoglobulin chimeric protein heterodimer complexes as
 PT platelet substitutes - contain the alpha and beta integrin chains
 PT associated in stable state and bind to extracellular matrix in the
 PT presence of plasma components

XX Example 10; Page 30; 87pp; Japanese.

XX

CC Sequences AAW70543 to AAW70545 represent CS-1 peptide fragments used
 CC during the course of the invention. The invention provides integrin-
 CC immunoglobulin chimeric protein heterodimer complexes that comprise an
 CC integrin alpha or beta chain associated with an immunoglobulin light or
 CC heavy chain. These chimeric proteins form heterodimer complexes, in
 CC particular with a chimeric protein containing an integrin alpha chain
 CC and an immunoglobulin chain with a chimeric protein containing an
 CC integrin beta chain and an immunoglobulin chain; the immunoglobulin chain
 CC in each case may be a heavy chain, or one of the two may be a light
 CC chain. The integrin alpha chain is preferably alpha 4 or alpha 2 and the
 CC integrin beta chain is preferably beta 1. Animal cells transformed with
 CC vectors containing the DNA coding for the above chimeric proteins can be
 CC used in the preparation of the chimeric proteins and their heterodimer
 CC complexes. The heterodimer complexes, which are useful for testing
 CC potential promoters and inhibitors of the binding of integrins to their
 CC ligands, function as blood platelet substitutes and hemostatics and as
 CC diagnostic agents.

XX Sequence 10 AA;

Query Match 100.0%; Score 23; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 31;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
 Db 3 EILDV 7

RESULT 48

AAW71246

ID AAW71246 standard; Peptide; 10 AA.

XX

XX AAW71246;

XX

DT 18-NOV-1998 (first entry)

XX Peptide sequence of the invention.

DE Hepatitis drug; integrin inhibitor; integrin binding; VLA-4; treatment;

XX Hepatitis.

XX Synthetic.

OS WO9837914-A1.

PN 03-SEP-1998.

PD 26-FEB-1998; 98WO-JP00802.

XX 26-FEB-1997; 97JP-0042493.

XX (TORA) TORAY IND INC.

XX Kainoh M, Moriya K, Tanaka T;

XX WPI; 1998-480938/41.

XX Integrin inhibitors including antibodies, proteins, nucleic acids,

PT saccharide(s), capable of binding to integrin(s) as active

PT ingredient in remedies - for treating hepatitis, by inhibiting cell

PT adhesion

XX Example 4; Page 19; 35pp; Japanese.

XX

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XX DE CS-1 peptide portion.

XX KW Cyclic CS-1 peptidomimetic inhibitor; Jurkat cell binding;

XX KW fibronectin CS-1 mediated inflammation; rheumatoid arthritis;

XX KW sVCAM 1/VLA-4 mediated inflammation; asthma; arthritic condition;

XX KW rheumatoid arthritis; osteoarthritis; allograft rejection; CS-1;

XX KW skin inflammation; demyelinating disease; central nervous system.

XX OS Synthetic.

XX OS US5869448-A.

XX PN 09-FEB-1999.

XX PF 25-AUG-1995; 95US-0519109.

XX PR 25-AUG-1995; 95US-0519109.

XX PR 25-AUG-1994; 94US-0296241.

XX PA (CYTE-) CYTEL CORP.

XX PI Arrhenius TS, Elices MJ, Tempczyk A, Zheng Z;

XX PI WPI; 1999-152837/13.

XX PT Cyclic inhibitor peptide - useful for treating fibronectin CS-1 or

XX PT sVCAM-1/VLA-4 mediated inflammation, e.g. asthma and arthritic

XX PT conditions

XX PS Example 8; Column 14; 47pp; English.

XX SS The present sequence represents part of a CS-1 peptide. The

XX SS specification describes a cyclic CS-1 peptidomimetic inhibitor peptide,

XX SS which is water soluble and inhibits the binding of Jurkat cells to a

XX SS solid-phase bound peptide (AAW8057). The inhibitor peptides are useful

XX SS for treating fibronectin CS-1 or sVCAM 1/VLA-4 mediated inflammation,

XX SS e.g. asthma, arthritic conditions (e.g. rheumatoid arthritis,

XX SS osteoarthritis), allograft rejection, skin inflammation and demyelinating

XX SS diseases of the central nervous system.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5

DB |||||

3 EILDV 7

RESULT 50

AAU77412

ID AAU77412 standard; peptide; 10 AA.

XX AC AAU77412;

XX AC 22-MAY-2000 (first entry)

XX DE Fibronectin CS1-derived peptide, SEQ ID NO:3.

XX KW Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;

XX KW CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;

XX KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.

XX OS Mammalia.

XX OS WO200002903-A1.

XX PN 20-JAN-2000.

XX PD 15-DEC-1998; 98WO-US26605.

XX PF

XX PR 10-JUL-1998; 98US-0113689.

XX PA (CYTE-) CYTEL CORP.

XX PI Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;

XX PI WPI; 2000-182213/16.

XX PT New peptidomimetic compounds used as cell surface fibronectin

XX PT expressing receptor and VLA-4 inhibitors for treating inflammatory and

XX PT cardiovascular disorders

XX PS Example 3; Page 238; 243pp; English.

XX SS The invention relates to peptidomimetic compounds (AAU77415-Y77438)

XX SS capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,

XX SS CD49d/CD29) to the CS-1 portion (25 amino acids) of a splice variant of

XX SS the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on

XX SS the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an

XX SS important role in the maturation and trafficking. VLA-4-mediated

XX SS leukocyte adhesion to the CS-1 FN of endothelial cells is also a

XX SS critical step in the inflammatory response. The peptidomimetics of the

XX SS invention may be used to treat both chronic and acute immunoinflammatory

XX SS conditions, such as asthma, rheumatoid arthritis, osteoarthritis and

XX SS allograft rejection. They may also be used to treat psoriasis and other

XX SS skin inflammations, demyelinating diseases of the central nervous system

XX SS (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,

XX SS diabetes, inflammatory bowel disease, kidney inflammation and

XX SS restenosis. Prior art inhibition of VLA-4/CS-1 interaction either

XX SS involves the use of anti-VLA-4 antibodies, which can themselves induce an

XX SS immune response on repeated administration, or the 25-mer CS-1 peptide,

XX SS which is large and costly to make and is subject to rapid proteolytic

XX SS degradation. The peptidomimetics of the invention are smaller in

XX SS comparison to the CS-1 peptide and therefore less expensive to

XX SS manufacture, and are resistant to proteolysis. Sequences AAU77411-Y77414

XX SS and AAU77434-Y77444 represent fragments of the CS-1 peptide tested for

XX SS their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide

XX SS (AAU77410).

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5

DB |||||

3 EILDV 7

RESULT 51

AAU74984

ID AAU74984 standard; Peptide; 10 AA.

XX AC AAU74984;

XX AC 09-APR-2002 (first entry)

XX DE Transfection associated, integrin binding peptide #8.

XX KW Virucide; human immunodeficiency virus; HIV; cytostatic;

XX KW ophthalmological; vasotropic; vaccine; gene therapy; transfection;

XX KW cystic fibrosis; asthma; cancer; leukaemia; glaucoma; gene vaccination;

XX KW anti-sense therapy; eye disease; corneal organ transplant; integrin;

XX KW transfection; restenosis.

XX OS Synthetic.

XX OS WO200192543-A2.

XX PN 06-DEC-2001.

XX PD

XX PF

PF 30-MAY-2001; 2001WO-GB02396.
XX
XX
PR 30-MAY-2000; 2000GB-0013089.
FR 30-MAY-2000; 2000GB-0013090.
XX 01-MAY-2001; 2001US-287410P.
XX
PA (ICHI-) ICH PRODN LTD.
XX
XX Hart SL;
XX WPI; 2002-114355/15.
DR
XX
XX
PT Transfecting confluent cells with nucleic acid for gene therapy or gene
PT vaccination, comprises contacting the cells with a receptor-targeted
PT vector having the nucleic acid and an agent that disrupts cell-cell
XX junctions -
XX
PS Claim 17; Page 17; 11pp; English.
XX
XX The invention describes transfecting (I) confluent cells or other slowly
CC dividing or non-dividing cells that are in contact with each other, with
CC a nucleic acid. The method comprises contacting the cells with a
CC receptor-targeted vector comprising the nucleic acid, and an agent that
CC disrupts cell-cell junctions under conditions suitable to effect
CC transfection. (I) is useful for transfecting bronchial and lung
CC epithelium for gene therapy for cystic fibrosis, asthma and also various
CC cancers and viral infections e.g. human immunodeficiency virus (HIV)
CC infection. Haematopoietic cell transfection enables gene therapy, gene
CC vaccination and anti-sense therapy of diseases involving haematopoietic
CC cells, including leukaemia and bone marrow stem cell disorders.
CC Transfection of corneal endothelium is useful for treatment of eye
CC disease affecting the cornea or corneal organ transplants, for e.g. in
CC glaucoma. A gene preventing cell proliferation in blood vessel walls is
CC introduced using an integrin targeting transfection vector complex (II)
CC to reduce restenosis. (II) is useful for intracellular transport and
CC delivery of anti-sense oligonucleotides, which enables antiviral and
CC cancer therapy and is effective in transporting large DNA molecules.
CC This sequence represents a peptide that lacks the conserved RGD
CC integrin binding amino acid sequence but binds integrins allowing the
CC nucleic acid to pass into the cell, described in the method of the
XX invention.
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 3 EILDV 7
RESULT 52
AAE17114
ID AAE17114 standard; peptide; 10 AA.
XX
XX AAE17114;
AC
XX
DT 18-APR-2002 (first entry)
XX
DE Integrin-binding peptide #16.
XX
XX Integrin binding component; polycationic nucleic acid-binding component;
KW lipid component; prophylaxis; immunisation; antisense therapy; asthma;
KW cystic fibrosis; cancer; viral infection; human immunodeficiency virus;
KW HIV infection; vaccine; neuroblastoma; bone marrow stem cell disorder;
KW leukaemia; adjuvant immunotherapy; eye disease; glaucoma; restenosis;
KW integrin-binding peptide.
XX
XX Unidentified.
OS
XX
XX
XX WO200192542-A2.
FN

XX
PD
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-GB02394.
XX
XX 30-MAY-2000; 2000GB-0013089.
PR 30-MAY-2000; 2000GB-0013090.
PR 01-MAY-2001; 2001US-287410P.
XX
XX (ICHI-) ICH PRODN LTD.
PA
XX Hart SL;
XX
XX WPI; 2002-139612/18.
DR
XX
XX
PT Complex for transfecting cell with nucleic acid for treating,
PT preventing conditions caused by deficiency in a gene in humans, has
PT nucleic acid, lipid, integrin binding and polycationic nucleic
PT acid-binding components -
XX
XX Claim 18; Page 78; 108pp; English.
PS
XX
XX The invention relates to integrin-targeting vectors having enhanced
CC transfection activity. The vector complex comprises a nucleic acid,
CC an integrin binding component, a polycationic nucleic acid-binding
CC component and a lipid component. The integrin binding component
CC comprises an integrin-binding element and a spacer element. Complex
CC of the invention is useful for transfecting cells in vitro or in
CC vivo with a nucleic acid, for treatment or prophylaxis of a condition
CC caused in human or a non-human animal by a defect and/or a deficiency
CC in a gene, immunisation and antisense therapy of a human or a non-human
CC animal. It is useful for transfecting bronchial and lung epithelium and
CC corneal endothelium for gene therapy for cystic fibrosis, asthma and
CC also various cancers and viral infections for example human
CC immunodeficiency virus (HIV) infection. It is also useful as a vaccine
CC or for therapy of neuroblastoma and the effective transfection of
CC primary smooth muscle cells, cardiac myocytes and haematopoietic cells.
CC Haematopoietic cell transfection enables gene therapy, gene vaccination
CC and antisense therapy of diseases involving haematopoietic cells,
CC including leukaemia and bone marrow stem cell disorders, for example
CC transfection of a cytokine gene may be useful for adjuvant immunotherapy.
CC Transfection of corneal endothelium is useful for treatment of eye
CC disease affecting the cornea or corneal organ transplants, for example
CC in glaucoma. A gene that prevents proliferation of cells in blood
CC vessel walls is introduced using complex of the invention to reduce
CC restenosis. The present sequence is integrin-binding peptide
XX of the invention.
SQ Sequence 10 AA;
Query Match 100.0%; Score 23; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 3 EILDV 7
RESULT 53
AAE92535
ID AAE92535 standard; peptide; 11 AA.
XX
XX AAE92535;
AC
XX
XX 09-SEP-1996 (first entry)
DT
XX
XX VIA-4 binding peptide #5.
DE
XX
XX VIA-4; inhibitor; binding peptide; leucocyte adhesion; CD49d/CD29; CDR;
KW alpha4beta1 integrin; VCAM-1; endothelial cell; antibody; meningitis;
KW complementarity determining region; inflammatory brain disorder; therapy;
KW multiple sclerosis; encephalitis; Alzheimer's disease; atherosclerosis;
KW

KW AIDS dementia; diabetes; inflammatory bowel disease; tumour metastases;
 KW rheumatoid arthritis; transplant rejection; myocardial ischaemia; asthma.
 XX Synthetic.
 XX WO9601644-A1.
 XX 25-JAN-1996.
 XX 10-JUL-1995; 95WO-US08516.
 XX 06-JUN-1995; 95US-0467580.
 XX 11-JUL-1994; 94US-0273055.
 XX (ATHE-) ATHENA NEUROSCIENCES INC.
 XX Pleiss MA, Thorsett BD, Yednock TA;
 XX WPI; 1996-097452/10.
 XX New peptide(s) that bind VLA-4, inhibit leucocyte adhesion - useful
 PT esp. for treatment of inflammatory disease, e.g. multiple sclerosis
 XX Example 5; Page 23; 42pp; English.
 XX AAR92534 and AAR92535 represents VLA-4 binding peptides. VLA-4 is also
 CC known as alpha4beta1 integrin and CD49d/CD29. VLA-4 binds to the
 CC non-matrix molecule VCAM-1, which is expressed by endothelial and other
 CC cells. This sequence (and peptides designed from it) mimic a short
 CC consensus sequence in the heavy chain complementarity determining region
 CC (CDR) 3 of monoclonal antibodies against alpha4beta1 integrin. This
 CC sequence inhibits the adhesion of leucocytes mediated by VLA-4. It is
 CC useful for treating inflammatory brain disorders (especially multiple
 CC sclerosis), meningitis, encephalitis, asthma, Alzheimer's disease,
 CC atherosclerosis, AIDS dementia, diabetes, inflammatory bowel disease,
 CC rheumatoid arthritis, transplant rejection, tumour metastases and
 CC myocardial ischaemia. This sequence can also be labelled, and can then
 CC be used for in vivo or in vitro diagnosis, such as monitoring
 CC inflammatory responses, isolating leucocytes, in assays for inhibitors of
 CC VLA-4/VCAM-1 interactions and imaging sites of inflammation.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 23; DB 17; Length 11;
 Best Local Similarity 100.0%; Pred. NO. 35;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db |||||
 4 EILDV 8
 RESULT 54
 AAW01704
 ID AAW01704 standard; peptide; 12 AA.
 XX
 AC AAW01704;
 XX
 DT 16-APR-1997 (first entry)
 XX
 DE B12 fibronectin peptide recognition sequence for VLA-4.
 KW fibronectin; high affinity; CS-1; recognition sequence; VLA-4;
 KW alpha-4 beta-1 cell adhesion receptor; CD49d/CD29; inhibitor;
 KW leukocyte trafficking function; peptidomimetic; treatment; asthma;
 KW rheumatoid arthritis; osteoarthritis; allograft rejection;
 KW skin inflammation; central nervous system demyelinating disease.
 XX Synthetic.
 XX WO9515973-A1.
 XX 15-JUN-1995.

XX 05-DEC-1994; 94WO-US13943.
 XX 02-DEC-1994; 94US-0164101.
 PR 06-DEC-1993; 93US-0164101.
 XX (CYTE-) CYTEL CORP.
 XX Arrhenius TS, Elices MJ, Gaeta FCA;
 PI WPI; 1995-224284/29.
 DR New peptide mimics of fibronectin CS-1 sequence - inhibit
 XX interaction of endothelial cells and VLA-4 carrying inflammatory
 PT cells, for treating or preventing asthma, arthritis etc.
 XX Disclosure; Page 78; 103pp; English.
 XX This sequence is a fragment of CS-1 (AAW01703) a high affinity peptide
 CC recognition sequence for VLA-4 within fibronectin. The alpha-4 beta-1
 CC (CD49d/CD29, VLA-4) cell adhesion receptor is an active participant in
 CC leukocyte trafficking functions. Binding of inflammatory cells to
 CC endothelial cells that express the CS-1 portion of FN on their surfaces
 CC can be inhibited by CS-1 peptidomimetic cpds. of minimal length. A
 CC minimal essential sequence for specific VLA-4 recognition of CS-1 has
 CC been identified as the tripeptide LDV. The generic peptidomimetic
 CC inhibits the binding of Jurkat cells (ATCC TIB 152) to a solid phase-
 CC bound CS-1 peptide in an in vitro assay in an aq. buffer at a pH value
 CC of 7.2-7.4 to an extent that is equal to or upto about 3000-fold greater
 CC than the inhibition in the binding exhibited by AAW01705. Deletion
 CC mutants of the present sequence were formed and in vitro binding of the
 CC peptides was assayed and compared to that of the full length CS-1
 CC peptide. CS-1 mediated inflammation, e.g. asthma, rheumatoid arthritis,
 CC osteoarthritis, allograft rejection, skin inflammation or central nervous
 CC system demyelinating disease, can be treated by the peptidomimetics. See
 CC AAW01708-27 for exemplary inhibitor peptides.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 23; DB 16; Length 12;
 Best Local Similarity 100.0%; Pred. NO. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db |||||
 5 EILDV 9
 RESULT 55
 AAW88061
 ID AAW88061 standard; peptide; 12 AA.
 XX
 AC AAW88061;
 XX
 DT 12-APR-1999 (first entry)
 XX
 DE B12 peptide sequence.
 XX
 KW Cyclic CS-1 peptidomimetic inhibitor; Jurkat cell binding;
 KW fibronectin CS-1 mediated inflammation; rheumatoid arthritis;
 KW sVCAM 1/VLA-4 mediated inflammation; asthma; arthritic condition;
 KW rheumatoid arthritis; osteoarthritis; allograft rejection;
 KW skin inflammation; demyelinating disease; central nervous system.
 XX Synthetic.
 OS US5869448-A.
 PN 09-FEB-1999.
 PD
 XX 25-AUG-1995; 95US-0519109.
 XX 25-AUG-1995; 95US-0519109.
 PR

PR 25-AUG-1994; 94US-0296241.
 PA (CYTE-) CYTEL CORP.
 PI Arrhenius TS, Elices MJ, Tempczyk A, Zheng Z;
 XX WPI; 1999-152837/13.
 XX
 XX Cyclic inhibitor peptide - useful for treating fibronectin CS-1 or
 PT sVCAM-1/VLA-4 mediated inflammation, e.g. asthma and arthritic
 PT conditions
 XX
 XX Disclosure; Columns 77-78; 47pp; English.
 XX
 XX The specification describes a cyclic CS-1 peptidomimetic inhibitor
 CC which is water soluble and inhibits the binding of Jurkat cells to a
 CC solid-phase bound peptide (AAW88057). The inhibitor peptides are useful
 CC for treating fibronectin CS-1 or sVCAM 1/VLA-4 mediated inflammation,
 CC e.g. asthma, arthritic conditions (e.g. rheumatoid arthritis,
 CC osteoarthritis), allograft rejection, skin inflammation and
 CC demyelinating diseases of the central nervous system. The present
 CC sequence appears in the specification.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 23; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db |||||
 5 EILDV 9
 RESULT 56
 ID AAW95414 standard; peptide; 12 AA.
 XX
 AC AAW95414;
 XX
 XX 18-MAR-1999 (first entry)
 DE Integrin-binding peptide.
 XX
 XX Integrin; transfection complex; integrin-binding; lipid; immunisation;
 KW antisense therapy, enzyme; therapeutic agent; immunogen; cystic fibrosis;
 KW cancer; viral infection; human immunodeficiency virus; cardiovascular;
 KW restenosis; leukaemia; asthma; glaucoma.
 XX
 OS Synthetic.
 XX
 XX WO9854347-A1.
 PN
 XX 03-DEC-1998.
 PD
 XX 29-MAY-1998; 98WO-GB01577.
 XX
 XX 29-MAY-1997; 97GB-0011115.
 XX
 XX (CHIL-) INST CHILD HEALTH.
 PA
 XX Hart SL;
 XX
 XX WPI; 1999-045366/04.
 XX
 XX New integrin-targeting transfection complex including lipid - used
 PT to improve transfection efficiency for a very wide range of cells,
 PT useful in, e.g. antisense therapy and genetic immunisation
 XX
 XX Claim 12; Page 50; 70pp; English.
 PS
 XX The invention relates to an integrin-targeting transfection complex. The
 CC complex comprises a nucleic acid, an integrin-binding component, a

CC polycationic nucleic acid-binding component and a lipid. The complexes
 CC are used for in vivo or in vitro transfection of cells, specifically:
 CC (i) for treatment or prevention of disease (in humans or other animals)
 CC caused by defective or deficient genes; (ii) for immunisation; (iii) for
 CC antisense therapy, and (iv) for protein production in host cells, e.g.
 CC of enzymes, therapeutic agents, vaccinating immunogens and diagnostic
 CC antigens. Typical of the diseases that can be treated or prevented are
 CC cystic fibrosis, cancer, viral infection (e.g. human immunodeficiency
 CC virus), cardiovascular disease (e.g. restenosis), leukaemia, asthma and
 CC glaucoma. Incorporation of the lipid into the complex increases
 CC transfection levels from 1-10 percent to over 50 percent. This effect is
 CC observed with all cell types tested including those that are resistant to
 CC transfection by most plasmid vectors. The complexes can carry large
 CC genes, up to 125 kb, e.g. an artificial chromosome. The present sequence
 CC represents a claimed example of an integrin-binding peptide used in the
 CC transfection complexes.
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 23; DB 20; Length 12;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db |||||
 5 EILDV 9
 RESULT 57
 ID AAY77411 standard; peptide; 12 AA.
 XX
 AC AAY77411;
 XX
 XX 22-MAY-2000 (first entry)
 DT
 XX Fibronectin CSI-derived peptide, SEQ ID NO:2.
 DE
 XX Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1;
 KW CD49c/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion;
 KW inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
 XX
 OS Mammalia.
 XX
 XX WO200002903-A1.
 PN
 XX 20-JAN-2000.
 PD
 XX 15-DEC-1998; 98WO-US26605.
 XX
 XX 10-JUL-1998; 98US-0113689.
 PR
 XX (CYTE-) CYTEL CORP.
 PA
 XX Arrhenius TS, Elices MJ, Gaeta FCA, He Y, Huyghe BG, Chen PG;
 PI WPI; 2000-182213/16.
 XX
 XX New peptidomimetic compounds used as cell surface fibronectin
 PT expressing receptor and VLA-4 inhibitors for treating inflammatory and
 PT cardiovascular disorders -
 PT
 XX Disclosure; Page 238; 243pp; English.
 PS
 XX The invention relates to peptidomimetic compounds (AAY77415-Y77438)
 CC capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1,
 CC CD49c/CD29) to the CS-1 portion (25 amino acids) of a splice variant of
 CC the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on
 CC the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an
 CC important role in the maturation and trafficking. VLA-4-mediated
 CC leukocyte adhesion to the CS-1 FN of endothelial cells is also a
 CC critical step in the inflammatory response. The peptidomimetics of the
 CC invention may be used to treat both chronic and acute immunoinflammatory

CC conditions, such as asthma, rheumatoid arthritis, osteoarthritis and
 CC allograft rejection. They may also be used to treat psoriasis and other
 CC skin inflammations, demyelinating diseases of the central nervous system
 CC (e.g., multiple sclerosis), allergies, atherosclerosis, colitis,
 CC diabetes, inflammatory bowel disease, kidney inflammation and
 CC restenosis. Prior art inhibition of VLA-4/CS-1 interaction either
 CC involves the use of anti-VLA-4 antibodies, which can themselves induce an
 CC immune response on repeated administration, or the 25-mer CS-1 peptide,
 CC which is large and costly to make and is subject to rapid proteolytic
 CC degradation. The peptidomimetics of the invention are smaller in
 CC comparison to the CS-1 peptide and therefore less expensive to
 CC manufacture, and are resistant to proteolysis. Sequences AAU77411-Y77414
 CC and AAU77434-Y77444 represent fragments of the CS-1 peptide tested for
 CC their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide
 CC (AAU77410).

XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 23; DB 21; Length 12;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 5 EILDV 9
 |||||

RESULT 58
 AAU74966

ID AAU74966 standard; Peptide; 12 AA.
 AC AAU74966;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Non-RGD containing alpha 4 beta 1 integrin binding peptide.
 XX
 KW Virucide; human immunodeficiency virus; HIV; cytostatic;
 KW ophthalmological; vasotropic; vaccine; gene therapy; transfection;
 KW cystic fibrosis; asthma; cancer; leukaemia; glaucoma; gene vaccination;
 KW anti-sense therapy; eye disease; corneal organ transplant; integrin;
 KW transfection; restenosis; alpha 4 beta 1 integrin.
 XX
 OS Synthetic.
 XX
 XX WO200192543-A2.
 XX
 XX 06-DEC-2001.
 XX
 PF 30-MAY-2001; 2001WO-GB02396.
 XX
 PR 30-MAY-2000; 2000GB-0013089.
 PR 30-MAY-2000; 2000GB-0013090.
 PR 01-MAY-2001; 2001US-287410P.
 XX
 PA (ICHI-) ICH PROD LTD.
 XX
 XX Hart SL;
 XX
 XX WPI; 2002-114355/15.
 DR
 XX
 PT Transfecting confluent cells with nucleic acid for gene therapy or gene
 PT vaccination, comprises contacting the cells with a receptor-targeted
 PT vector having the nucleic acid and an agent that disrupts cell-cell
 PT junctions
 XX
 PS Disclosure; Page 15; 11pp; English.
 XX
 CC The invention describes transfecting (i) confluent cells or other slowly
 CC dividing or non-dividing cells that are in contact with each other, with
 CC a nucleic acid. The method comprises contacting the cells with a
 CC receptor-targeted vector comprising the nucleic acid, and an agent that
 CC disrupts cell-cell junctions under conditions suitable to effect

CC transfection. (i) is useful for transfecting bronchial and lung
 CC epithelium for gene therapy for cystic fibrosis, asthma and also various
 CC cancers and viral infections e.g. human immunodeficiency virus (HIV)
 CC infection. Haematopoietic cell transfection enables gene therapy. Gene
 CC vaccination and anti-sense therapy of diseases involving haematopoietic
 CC cells, including leukaemia and bone marrow stem cell disorders.
 CC transfection of corneal endothelium is useful for treatment of eye
 CC disease affecting the cornea or corneal organ transplants, for e.g. in
 CC glaucoma. A gene preventing cell proliferation in blood vessel walls is
 CC introduced using an integrin targeting transfection vector complex (ii)
 CC to reduce restenosis. (ii) is useful for intracellular transport and
 CC delivery of anti-sense oligonucleotides, which enables antiviral and
 CC cancer therapy and is effective in transporting large DNA molecules.
 CC This sequence represents a peptide that lacks the conserved RGD
 CC amino acid sequence and cysteine residues for cyclisation, but can
 CC bind to integrins to allow the nucleic acid to pass into the cell,
 CC described in the method of the invention.

XX
 SQ Sequence 12 AA;

Query Match 100.0%; Score 23; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
 Db 5 EILDV 9
 |||||

RESULT 59
 AAU17104

ID AAU17104 standard; peptide; 12 AA.
 AC AAU17104;
 XX
 DT 18-APR-2002 (first entry)
 XX
 DE Integrin-binding peptide 7.
 XX
 KW Integrin binding component; polycationic nucleic acid-binding component;
 KW lipid component; prophylaxis; immunisation; anti-sense therapy; asthma;
 KW cystic fibrosis; cancer; viral infection; human immunodeficiency virus;
 KW HIV infection; vaccine; neuroblastoma; bone marrow stem cell disorder;
 KW leukaemia; adjuvant immunotherapy; eye disease; glaucoma; restenosis;
 KW integrin-binding peptide.
 XX
 OS Unidentified.
 XX
 XX WO200192542-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 30-MAY-2001; 2001WO-GB02394.
 XX
 PF 30-MAY-2000; 2000GB-0013089.
 PR 30-MAY-2000; 2000GB-0013090.
 PR 01-MAY-2001; 2001US-287410P.
 XX
 XX (ICHI-) ICH PROD LTD.
 XX
 XX Hart SL;
 PI
 XX WPI; 2002-139612/18.
 DR
 XX
 PT Complex for transfecting cell with nucleic acid for treating,
 PT preventing conditions caused by deficiency in a gene in humans, has
 PT nucleic acid, lipid, integrin binding and polycationic nucleic
 PT acid-binding components
 XX
 PS Disclosure; Page 7; 108pp; English.
 XX
 CC The invention relates to integrin-targeting vectors having enhanced
 CC transfection activity. The vector complex comprises a nucleic acid,

an integrin binding component, a polycationic nucleic acid-binding component and a lipid component. The integrin binding component comprises an integrin-binding element and a spacer element. Complex of the invention is useful for transfecting cells in vitro or in vivo with a nucleic acid, for treatment or prophylaxis of a condition caused in human or a non-human animal by a defect and/or a deficiency in a gene, immunisation and antitense therapy of a human or a non-human animal. It is useful for transfecting bronchial and lung epithelium and corneal endothelium for gene therapy for cystic fibrosis, asthma and also various cancers and viral infections for example human immunodeficiency virus (HIV) infection. It is also useful as a vaccine or for therapy of neuroblastoma and the effective transfection of primary smooth muscle cells, cardiac myocytes and haematopoietic cells. Haematopoietic cell transfection enables gene therapy, gene vaccination and antitense therapy of diseases involving haematopoietic cells, including leukaemia and bone marrow stem cell disorders, for example transfection of a cytokine gene may be used for adjuvant immunotherapy. Transfection of corneal endothelium is useful for treatment of eye disease affecting the cornea or corneal organ transplants, for example in glaucoma. A gene that prevents proliferation of cells in blood vessel walls is introduced using complex of the invention to reduce restenosis. The present sequence is integrin-binding peptide of the invention. This peptide is specific for alpha4beta1 integrin.

Query Match 100.0%; Score 23; DB 23; Length 12;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
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|
DB 5 EILDV 9

RESULT 60
AAW70541
ID AAW70541 standard; peptide; 13 AA.
AC AAW70541;
XX
XX 26-JAN-1999 (first entry)
XX
XX CS-1 peptide sequence (a fibronectin fragment).
DE Integrin; alpha-4 chain; immunoglobulin; chimeric; heterodimer complex;
KW inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
KW CS-1; fibronectin.
XX
XX Synthetic.
OS
PN WO9832771-A1.
XX
XX 30-JUL-1998.
XX
XX 29-JAN-1998; 98WO-JP00370.
XX
XX 29-AUG-1997; 97JP-0234544.
PR 29-JAN-1997; 97JP-0015118.
XX
XX (TORA) TORAY IND INC.
PA
XX Kainoh M, Tanaka T;
PI
XX WPI; 1998-427881/36.
XX
XX Integrin-immunoglobulin chimeric protein heterodimer complexes as
PT platelet substitutes - contain the alpha and beta integrin chains
PT associated in stable state and bind to extracellular matrix in the
PT presence of plasma components
XX
XX Claim 41; Page 25; 87pp; Japanese.

CC This represents a CS-1 peptide sequence. The invention provides
CC integrin-immunoglobulin chimeric protein heterodimer complexes that
CC comprise an integrin alpha or beta chain associated with an form
CC immunoglobulin light or heavy chain. These chimeric proteins form
CC heterodimer complexes, in particular with a chimeric protein containing
CC an integrin alpha chain and an immunoglobulin chain with a chimeric
CC protein containing an integrin beta chain and an immunoglobulin chain;
CC the immunoglobulin chain in each case may be a heavy chain, or one of the
CC two may be a light chain. The integrin alpha chain is preferably alpha 4
CC or alpha 2 and the integrin beta chain is preferably beta 1. Animal cells
CC transformed with vectors containing the DNA coding for the above chimeric
CC proteins can be used in the preparation of the chimeric proteins and
CC their heterodimer complexes. The heterodimer complexes, which are useful
CC for testing potential promoters and inhibitors of the binding of
CC integrins to their ligands, function as blood platelet substitutes and
CC hemostatics and as diagnostic agents.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 23; DB 19; Length 13;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
|
|
|
|
|
DB 6 EILDV 10

RESULT 61
AAW71245
ID AAW71245 standard; Peptide; 13 AA.
XX
XX AAW71245;
AC
XX 18-NOV-1998 (first entry)
DT
XX Peptide sequence of the invention.
DE
XX Hepatitis drug; integrin inhibitor; integrin binding; VLA-4; treatment;
KW hepatitis.
XX
XX Synthetic.
OS
PN WO9837914-A1.
XX
XX 03-SEP-1998.
PD
XX 26-FEB-1998; 98WO-JP00802.
PF
XX 26-FEB-1997; 97JP-0042493.
PR
XX (TORA) TORAY IND INC.
PA
XX Kainoh M, Moriya K, Tanaka T;
PI
XX WPI; 1998-480938/41.
DR
XX Integrin inhibitors including antibodies, proteins, nucleic acids,
PT saccharide(s), capable of binding to integrin(s) as active
PT ingredient in remedies - for treating hepatitis, by inhibiting cell
PT adhesion
XX
XX Example 3; Page 16; 35pp; Japanese.
PS
XX The present sequence is used in the course of the invention. The
CC specification describes Hepatitis drugs which contain integrin
CC inhibitors as the active ingredient. These integrin inhibitors include
CC antibodies, proteins, polypeptides, peptides, nucleic acids, saccharides,
CC and their derivatives. They also include low molecular weight compounds
CC capable of binding to integrins (e.g. alpha chain type with alpha 1,
CC alpha 2, etc., or beta chain type with beta 1, beta 2, etc.),
CC particularly anti-VLA-4 antibody, VLA-4 inhibiting peptides and low
CC molecular weight VLA-4 inhibiting compounds. The products can be used

CC for treating hepatitis.

SQ Sequence 13 AA;

Query Match 100.0%; Score 23; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

Db 6 EILDV 10

RESULT 62

ID AAY22632 standard; peptide; 13 AA.

XX AC AAY22632;

DT 12-AUG-1999 (first entry)

XX SEQ ID 57 of W09925731.

Cyclic hexapeptide; very late antigen-4; VLA-4; adhesion inhibitor;
inflammation; allergic inflammation; hepatitis; autoimmune disease;
rejection reaction; organ transplant; type I diabetes; Crohn's disease;
post-surgical restenosis; arteriosclerosis.

XX OS Synthetic.

XX PN W09925731-A1.

XX PD 27-MAY-1999.

XX PF 12-NOV-1998; 98WO-JP05096.

XX PR 13-NOV-1997; 97JP-0311692.

XX PA (TORA) TORAY IND INC.

XX PI Kainoh M, Saito N, Takahashi T, Takeshige H, Tanaka T;

XX WPI; 1999-370745/31.

XX New cyclic hexapeptides for treating inflammation and hepatitis

XX Example 4; Page 20; 45pp; Japanese.

The specification describes cyclic hexapeptides which are
are cyclised via disulphide or amide bonds. The peptides are
very late antigen-4 (VLA-4) adhesion inhibitors. They are
useful for treating inflammation, especially allergic inflammation
and hepatitis, autoimmune disease, rejection reactions following organ
transplants, type I diabetes, Crohn's disease, post-surgical restenosis
and arteriosclerosis. The present sequence is used in the course of
the invention.

SQ Sequence 13 AA;

Query Match 100.0%; Score 23; DB 20; Length 13;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

Db 6 EILDV 10

RESULT 63

ID AAB70683 standard; peptide; 13 AA.

XX AC AAB70683;

XX

DT 16-MAY-2001 (first entry)

XX Synthetic CS-1 peptide.

Heterocyclic amide; cell adhesion inhibitor; very late antigen-4;
VLA-4 antagonist; antiasthmatic; antiallergic; antiinflammatory;
neuroprotective; antiarteriosclerotic; asthma; allergic rhinitis;
multiple sclerosis; atherosclerosis; inflammatory bowel disease.

XX OS Synthetic.

XX PN W0200112183-A1.

XX PD 22-FEB-2001.

XX PF 14-AUG-2000; 2000WO-US22115.

XX PR 16-AUG-1999; 99US-0149042.

XX PA (MERI) MERCK & CO INC.

XX Haggmann WK, Delaszlo SE, Doherty G, Chang LL, Yang GX;

XX WPI; 2001-168836/17.

Use of new and known heterocyclic amides as VLA-4 antagonists to treat
and prevent disorders mediated by cell adhesion e.g. asthma, allergic
rhinitis, multiple sclerosis, atherosclerosis and inflammatory bowel
disease -

XX Example 198; Page 148; 169pp; English.

The present invention describes heterocyclic amides (I) which are used
as very late antigen-4 (VLA-4) antagonists to treat diseases mediated
by cell adhesion. (I) has antiasthmatic, antiallergic, antiinflammatory,
neuroprotective and antiarteriosclerotic activities. (I) are used to
prevent the action of VLA-4 in prevention and treatment of diseases
mediated by cell adhesion selected from asthma, allergic rhinitis,
multiple sclerosis, atherosclerosis and inflammatory bowel disease.
The present sequence represents a synthetic CS-1 peptide which is used
in an example from the present invention.

SQ Sequence 13 AA;

Query Match 100.0%; Score 23; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

Db 6 EILDV 10

RESULT 64

ID AAU77526 standard; Peptide; 13 AA.

XX AC AAU77526;

DT 05-JUN-2002 (first entry)

XX Very late antigen-4 (VLA-4) dependent adhesion related peptide, CS-1.

Very late antigen-4; VLA-4; cell adhesion inhibitor; CD49d/CD29;
alpha4/beta7 integrin; cyclic amide derivative; rhinitis; asthma;
multiple sclerosis; atherosclerosis; bowel disease; inflammation;
nephritis; AIDS-related dementia; acquired immunodeficiency syndrome;
diabetes; conjunctivitis; Alzheimer's disease; aortic stenosis; myeloma;
contact dermal hypersensitivity; ulcerative colitis; Crohn's disease;
lung disease; cancer; viral infection; meningitis; pulmonary fibrosis;
myocarditis; organ transplantation; psoriasis; restenosis; retinitis;
arthritis; stroke; tumour metastasis; uveitis; vascular occlusion;

angioplasty.
 Synthetic.
 US2002010199-A1.
 24-JAN-2002.
 21-MAY-2001; 2001US-0862194.
 22-MAY-2000; 2000US-206183P.
 (HAGM/) HAGMANN W K.
 (DOHE/) DOHERTY G A.
 (SHAH/) SHAH S.
 Hagmann WK, Doherty GA, Shah S;
 WPI; 2002-215831/27.
 New substituted cyclic amidine derivatives for the prevention or
 treatment of disease mediated by cell adhesion in a mammal e.g. asthma
 -
 Example 2; Page 16; 22pp; English.
 The invention describes novel substituted cyclic amidine derivatives (I).
 (I) are useful for the prevention or treatment of disease or disorders
 mediated by cell adhesion in a mammal e.g. asthma, allergic rhinitis,
 multiple sclerosis, atherosclerosis, inflammatory bowel disease or
 inflammation e.g. acute respiratory distress syndrome (ARDS),
 AIDS-related dementia, allergic conjunctivitis, Alzheimer's disease,
 aortic stenosis, autologous bone marrow transplantation, certain types of
 toxic and immune based nephritis, contact dermal hypersensitivity,
 ulcerative colitis, Crohn's disease, inflammatory lung disease,
 inflammatory sequelae of viral infections, meningitis, multiple myeloma,
 myocarditis, organ transplantation, psoriasis, pulmonary fibrosis,
 restenosis, retinitis, rheumatoid arthritis, septic arthritis, stroke,
 cancer, tumour metastasis, uveitis, type 1 diabetes and vascular
 occlusion following angioplasty. The compound inhibits cell adhesion
 processes including cell activation, migration, proliferation and
 differentiation. This sequence represents the CS-1 peptide used to study
 the inhibition of very late antigen-4 (VLA-4, CD49d/CD29 or alpha4/beta7
 integrin) dependent adhesion.
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 23; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db |||||
 6 EILDV 10
 RESULT 65
 AAU98858
 ID AAU98858 standard; Peptide; 15 AA.
 XX AC
 AC AAU98858;
 DT 22-AUG-2002 (first entry)
 XX Human HSIJ immunogenic peptide #1.
 DE
 XX Immunogenic peptide; heat shock protein; HSP; DNAJ; immunomodulatory;
 KW cytosolic; antiinflammatory; antibacterial; antiarthritic; human;
 KW autoimmune disease; arthritis; articular juvenile idiopathic arthritis;
 KW infectious disease; inflammatory bowel disease; cancer; HSIJ;
 KW mucosal toleration; DNA vaccination; anergy induction.
 XX
 OS Homo sapiens.

XX WO200236611-A2.
 PN
 XX
 PD 10-MAY-2002.
 XX
 PF 31-OCT-2001; 2001WO-US45344.
 XX
 PR 01-NOV-2000; 2000US-245181P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (MART/) MARTINI A.
 XX Martini A, Albani S, Carson DA, Prakken BJ;
 DR WPI; 2002-489999/52.
 XX
 PT New immunomodulatory peptides from heat shock proteins, useful for
 treating immunological disorder in subjects such as humans, e.g.
 PT autoimmune disease (e.g. arthritis), infectious disease, inflammatory
 PT bowel disease or cancer -
 XX
 PS Claim 10; Page 56; 84pp; English.
 XX
 CC This invention relates to the use of a peptide, which is an immunogenic
 CC portion derived from a dnaJ heat shock protein (hsp) in modulating an
 CC immune response in a subject. The peptides of the invention may have
 CC immunomodulatory, cytostatic, antiinflammatory, antibacterial or
 CC antiarthritic properties and can stimulate expression of interleukins,
 CC tumour necrosis factor and transforming growth factor beta. The
 CC immunogenic peptide is useful for modulating (i.e. augmenting/inducing
 CC or reducing/inhibiting) an immune response in a subject having an
 CC immunological disorder (e.g. autoimmune disease such as arthritis or
 CC articular juvenile idiopathic arthritis), an infectious disease,
 CC an inflammatory bowel disease or cancer. The immunogenic peptide of
 CC the invention is also useful for modulating immunoeffector cell
 CC responsiveness in a subject. The immunogenic peptide is particularly
 CC useful for treating the above-mentioned diseases in mammals, e.g. cat,
 CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In
 CC general, the peptide is useful in methods involving mucosal
 CC toleration, DNA vaccination, anergy induction or active immunisation.
 CC The present sequence represents a human heat shock protein immunogenic
 CC peptide of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 23; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EILDV 5
 Db |||||
 5 EILDV 9
 RESULT 66
 AAR29632
 ID AAR29632 standard; peptide; 16 AA.
 XX AC
 AC AAR29632;
 XX
 DT 26-JAN-1993 (first entry)
 XX
 DE Adhesion inhibitor peptide #2.
 XX
 KW Triazine; polyethylene glycol; agglutination.
 OS Synthetic.
 XX JP04187698-A.
 PN
 XX 06-JUL-1992.
 PD
 XX
 PF 21-NOV-1990; 90JP-0316441.

CC inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many
CC different forms of osteoporosis, also for diagnosis. Attaching the
CC vehicle (especially Fc domain) to (I) increases the half-life (free (I)
CC are normally degraded very quickly in vivo). The present sequence
CC is an antagonist peptide of the invention.

XX
XX
SQ Sequence 19 AA; Query Match 100.0%; Score 23; DB 23; Length 19;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 EILDV 5
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|
Db 5 EILDV 9

RESULT 70
AAU81185 ID AAU81185 standard; Peptide; 19 AA.
XX AC AAU81185;
XX DT 09-APR-2002 (first entry)
XX DE Laminin-related peptide #16.
XX IGF Fc; anticoagulant; thrombolytic; cytostatic;
KW antiinflammatory; immunosuppressive; osteopathic; antagonist;
KW laminin; saw-scaled viper; echistatin; integrin; selectin; vinculin;
KW platelet aggregation; angiogenesis; tumour; inflammation;
KW autoimmune disease; rheumatoid arthritis; osteoporosis.
XX
XX Synthetic.
XX WO200181377-A2.
XX 01-NOV-2001.
XX 23-APR-2001; 2001WO-US13069.
XX 21-APR-2000; 2000US-198919P.
XX 03-MAY-2000; 2000US-201394P.
XX (AMGE-) AMGEN INC.
XX Feige U, Kohno T, Lacey DL, Boone TC;
XX WPI; 2002-062025/08.
XX Composition comprising integrin or adhesion antagonistic peptide and
XX vehicle, useful for treating or preventing platelet aggregation, has a
XX longer half-life than free peptide -
XX
XX Claim 13; Page 21; 68pp; English.

CC The invention relates to a composition comprising an integrin/adhesion
CC antagonistic peptide (I) and a vehicle e.g. IGG Fc. The peptides
CC are based on laminin or saw-scaled viper echistatin and target integrin,
CC selectin or vinculin. Also included are compounds of formula (Ia) and
CC their multimers (Xⁿ1_a-Fⁿ1-(Xⁿ2)_b where;
CC Fⁿ1 = Fc domain;
CC Xⁿ1 and Xⁿ2 = -(Lⁿ1)_c-pⁿ1, (Lⁿ1)_c-pⁿ1-(Lⁿ2)_d-pⁿ2,
CC (Lⁿ1)_c-pⁿ1-(Lⁿ2)_d-pⁿ2-(Lⁿ3)_e-pⁿ3 or
CC (Lⁿ1)_c-pⁿ1-(Lⁿ2)_d-pⁿ2-(Lⁿ3)_e-pⁿ3-(Lⁿ4)_f-pⁿ4;
CC pⁿ1-pⁿ4 = same or different (I);
CC Lⁿ1-Lⁿ4 = same or different linkers;
CC a-f = 0 or 1, provided at least one of a and b = 1,
CC a nucleic acid that encodes (Ia), an expression vector containing the
CC nucleic acid, host cells containing the vector, producing a
CC pharmacologically active compound (B) by covalently linking at least one
CC Fc domain to at least one amino acid sequence of a selected randomized
CC (I) and any of six laminin-related peptides (Ib). The compositions are

CC used prophylactically and therapeutically in the same way as (I), e.g. to
 CC inhibit platelet aggregation or angiogenesis (tumours), or to treat
 CC inflammation and autoimmune diseases (e.g. rheumatoid arthritis) and many
 CC different forms of osteoporosis, also for diagnosis. Attaching the
 CC vehicle (especially Fc domain) to (I) increases the half-life (free (I)
 CC are normally degraded very quickly in vivo). The present sequence
 CC is an antagonist peptide of the invention.

XX SQ Sequence 19 AA;

Query Match 100.0%; Score 23; DB 23; Length 19;

Best Local Similarity 100.0%; Pred. No. 64;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5

Db 10 EILDV 14

RESULT 71

AAR26821
 ID AAR26821 standard; peptide; 20 AA.

XX AC AAR26821;

XX DT 09-FEB-1993 (first entry)

XX DE Cell adhesion polypeptide.

XX KW MOLT-4; human; lymphoblastic leukaemia; A375-SM; metastatic;
 XX melanoma; H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease;
 XX rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Region 6..8

XX FT /note= "LDV region followed by Phe at position 17."

XX PN WO9213887-A.

XX PD 20-AUG-1992.

XX PF 06-FEB-1992; 92WO-GB00226.

XX PR 07-FEB-1991; 91GB-0002655.

XX PR 08-FEB-1991; 91GB-0002818.

XX PA (UYMA-) UNIV VICTORIA MANCHESTER.

XX PI Humphries MJ;

XX DR WPI; 1992-299988/36.

XX PT New cell adhesion (poly)peptide(s) modifying cell adhesive

XX PT properties - useful in treating inflammatory conditions e.g.

XX PT rheumatoid arthritis, asthma, inflammatory bowel disease, sepsis,

XX PT etc.

XX PS Disclosure; Page 4; 23pp; English.

XX CC The peptide is an example of a cell adhesion polypeptide contg. the

XX CC amino sequence X-Asp-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or

XX CC Val, A= any amino acid and n= 3-10. At least a subsequence of the

XX CC polypeptide is adherent for MOLT-4 human lymphoblastic leukaemia,

XX CC A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells.

XX CC The cell adhesion peptides are used to modify or control the

XX CC adhesive properties of cells, e.g. in treatment of inflammatory

XX CC conditions such as rheumatoid arthritis, asthma, sepsis, graft

XX CC rejection, inflammatory bowel disease, reperfusion of cardiac tissue

XX CC after myocardial infarction, and coagulatory disorders. They are

XX CC selective antagonists of cell adhesion, e.g. they promote adhesion

XX CC of the specified cells but inhibit adhesion to the natural adhesion

CC protein contg. the adhesive sequence.
 CC See also AAR26822-30 and AAR30887-903.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 23; DB 13; Length 20;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EILDV 5

Db 4 EILDV 8

RESULT 72

AAR30901

ID AAR30901 standard; peptide; 20 AA.

XX AC AAR30901;

XX DT 09-FEB-1993 (first entry)

XX DE Cell adhesion polypeptide CS12.

XX KW MOLT-4; human; lymphoblastic leukaemia; A375-SM; metastatic;
 XX melanoma; H1080; fibrosarcoma; LDV; LDL; IDA; inflammatory disease;
 XX rheumatoid arthritis; asthma; sepsis; graft rejection; reperfusion.

XX OS Synthetic.

XX PN WO9213887-A.

XX PD 20-AUG-1992.

XX PF 06-FEB-1992; 92WO-GB00226.

XX PR 07-FEB-1991; 91GB-0002655.

XX PR 08-FEB-1991; 91GB-0002818.

XX PA (UYMA-) UNIV VICTORIA MANCHESTER.

XX PI Humphries MJ;

XX DR WPI; 1992-299988/36.

XX PT New cell adhesion (poly)peptide(s) modifying cell adhesive

XX PT properties - useful in treating inflammatory conditions e.g.

XX PT rheumatoid arthritis, asthma, inflammatory bowel disease, sepsis,

XX PT etc.

XX PS Disclosure; Page 11; 23pp; English.

XX CC The peptide is an example of a cell adhesion polypeptide contg. the

XX CC amino sequence X-Asp-Y-(A)n-Phe, where X and Y = Ala, Leu, Ile or

XX CC Val, A= any amino acid and n= 3-10. At least a subsequence of the

XX CC polypeptide is adherent for MOLT-4 human lymphoblastic leukaemia,

XX CC A375-SM human metastatic melanoma or H1080 human fibrosarcoma cells.

XX CC The cell adhesion peptides are used to modify or control the

XX CC adhesive properties of cells, e.g. in treatment of inflammatory

XX CC conditions such as rheumatoid arthritis, asthma, sepsis, graft

XX CC rejection, inflammatory bowel disease, reperfusion of cardiac tissue

XX CC after myocardial infarction, and coagulatory disorders. They are

XX CC selective antagonists of cell adhesion, e.g. they promote adhesion

XX CC of the specified cells but inhibit adhesion to the natural adhesion

XX CC protein contg. the adhesive sequence.

XX CC See also AAR26821-30 and AAR30887-903.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 23; DB 13; Length 20;

Best Local Similarity 100.0%; Pred. No. 67;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 EILDV 5
   |||||
Db 5 EILDV 9

RESULT 73
AAW56047
ID AAW56047 standard; peptide; 21 AA.
XX
AC AAW56047;
XX
XX
DT 29-JUL-1998 (first entry)
XX
DE Alpha4 Integrins targeting sequence SEQ ID NO:57.
XX
KW Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW constrained peptide motif; gene therapy; cancer; heart disease;
KW autoimmune disorder.
XX
OS Synthetic.
OS Mastadenovirus.
XX
XX WO9807865-A1.
XX
XX 26-FEB-1998.
XX
XX Chimeric adenovirus fiber protein non-native amino acid sequence 59.
XX
XX Chimeric; adenovirus; fiber protein; binding; targeting; coat protein;
KW constrained peptide motif; gene therapy; cancer; heart disease;
KW autoimmune disorder.
XX
XX Synthetic.
OS Mastadenovirus.
XX
XX WO9807865-A1.
XX
XX 26-FEB-1998.
XX
XX 21-AUG-1997; 97WO-US14719.
XX
XX 21-AUG-1996; 96US-0701124.
XX
XX (GENV-) GENVEC INC.
XX
XX Kovesdi I, Roelvink PW, Wickham TJ;
XX WPI; 1998-169169/15.
XX
XX Chimeric adenovirus fibre proteins - containing non-native amino
PT acid sequence to provide for binding and entry into cells,
PT especially for gene therapy
XX
XX Example 8; Page 57; 124pp; English.
XX
XX The present sequence represents an alpha4 integrins targeting sequence,
CC which is used in an example from the present invention. The present
CC invention describes a chimeric adenovirus fibre protein (AFP) containing
CC a constrained non-native amino acid sequence. The non-native amino acid
CC sequence allows the chimeric fibre (or a vector comprising the chimeric
CC fibre) to more efficiently bind to and enter cells. The products can be
CC used for gene therapy, for treating cancer, e.g. melanoma, glioma and
CC lung cancers as well as genetic disorders, e.g. cystic fibrosis,
CC haemophilia and muscular dystrophy as well as pathogenic infections,
CC e.g. HIV, tuberculosis and hepatitis and also for heart disease, to e.g.
CC prevent restenosis following angioplasty or to promote angiogenesis to
CC reperfuse necrotic tissue, and in autoimmune disorders, e.g. Crohn's
CC disease, colitis, rheumatoid arthritis, and Alzheimer's disease.
XX
XX SQ Sequence 21 AA;
   Query Match 100.0%; Score 23; DB 19; Length 21;
   Best Local Similarity 100.0%; Pred. No. 71;
   Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
   |||||
Db 1 EILDV 5

RESULT 75
AAV13421
ID AAV13421 standard; peptide; 23 AA.
XX
XX
AC AAV13421;
XX
XX
DT 19-JUL-1999 (first entry)
XX
DE Conjugated control peptide L-B1.
XX
XX Immunogenic; conjugated polypeptide; herpes simplex virus; HSV; ICP4;
KW immunomodulatory; I cell; immunogen; vaccine; ICP27; glycoprotein B;
KW ribonucleotide reductase; ICP34.5; glycoprotein E; glycoprotein F;
KW immune response; genetic immunisation.
XX
XX Synthetic.
XX

```



```
PN WO9916710-A1.
XX
PD 08-APR-1999.
XX
PF 29-SEP-1998; 98WO-US20681.
XX
PR 30-SEP-1997; 97US-0060422.
XX
PA (CELS-) CEL-SCI CORP.
PA (UYNE-) UNIV NORTHEASTERN OHIO.
XX
PI Rosenthal KS, Zimmerman DH;
XX
DR WPI; 1999-312418/26.
XX
PT New immunogenic conjugated polypeptides
PS Example 1; Page 33; 69pp; English.
XX
CC The invention provides immunogenic conjugated polypeptides which comprise
CC a herpes simplex virus peptide (HSV) linked to an immunomodulatory
CC peptide and which promote binding to T cells. The novel immunogenic
CC conjugated polypeptides are effective as an immunogen in a vaccine for
CC treatment or prevention of infection by HSV and are represented by the
CC formula P1-X-P2 or P2-X-P1; where P1 = a HSV specific antigenic peptide
CC from a protein of HSV type 1 or type 2, selected from ICP27, glycoprotein
CC B, ribonucleotide reductase, ICP4, ICP34.5, glycoprotein E and
CC glycoprotein F; P2 = an immunomodulatory peptide which is a portion of
CC an immunoprotein which promotes binding to a class of subclass of T cells
CC and which directs a predominantly TH1 type immune response to the peptide
CC P1; and x = a covalent bond or a cleavable or non-cleavable peptide
CC linking group. The conjugated polypeptides can elicit an immune response
CC for neutralizing HSV and killing HSV infected cells. They can be used for
CC the treatment or prevention of HSV infection. In addition, DNA encoding
CC the polypeptide can be used for genetic immunization. They can also be
CC used to diagnose the presence of infection, active or latent, in an
CC individual by HSV by mixing T cells from the individual with the
CC polypeptide and detecting a reaction between the T cells and the
CC polypeptide.
XX
SQ Sequence 23 AA;
Query Match 100.0%; Score 23; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
Db 5 EILDV 9
|||||
Search completed: February 8, 2003, 10:23:45
Job time : 38 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:24:48 ; Search time 11 Seconds
(without alignments)
10.077 Million cell updates/sec

Title: US-09-251-073A-16
Perfect score: 23
Sequence: 1 EILDV 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 2216297 residues

Total number of hits satisfying chosen parameters: 28

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	5	9	US-10-086-217-6
2	23	100.0	5	9	US-09-320-907B-3
3	23	100.0	7	10	US-09-969-192-80
4	23	100.0	8	9	US-10-086-217-5
5	23	100.0	8	10	US-09-969-192-56
6	23	100.0	12	9	US-10-137-435-14
7	23	100.0	19	9	US-09-840-277-95
8	23	100.0	19	9	US-09-840-277-96
9	23	100.0	19	9	US-09-840-277-133
10	23	100.0	21	10	US-09-969-192-57
11	23	100.0	21	10	US-09-969-192-59
12	23	100.0	25	9	US-09-840-277-119
13	23	100.0	25	10	US-09-010-714-11
14	23	100.0	34	10	US-09-969-192-76
15	23	100.0	152	10	US-09-925-301-900
16	23	100.0	227	9	US-09-738-626-5384
17	23	100.0	344	9	US-09-738-626-4085
18	23	100.0	366	10	US-09-815-242-10394
19	23	100.0	366	10	US-09-815-242-13921

Sequence 14, Appl
Sequence 700, App
Sequence 6313, Ap
Sequence 492, App
Sequence 6019, Ap
Sequence 13659, A
Sequence 23, Appl
Sequence 9, Appl
Sequence 5, Appl

20 23 100.0 394 12 US-10-029-654-14
21 23 100.0 417 10 US-09-925-302-700
22 23 100.0 418 9 US-09-738-626-6313
23 23 100.0 560 10 US-09-841-132-492
24 23 100.0 706 9 US-09-738-626-6019
25 23 100.0 737 10 US-09-815-242-13699
26 23 100.0 784 9 US-10-145-014-23
27 23 100.0 813 8 US-08-910-386A-9
28 23 100.0 596 8 US-08-910-386A-5

ALIGNMENTS

RESULT 1
US-10-086-217-6
; Sequence 6, Application US/10086217
; Patent No. US2002015998A1
; GENERAL INFORMATION:
; APPLICANT: MUNDY, GREGORY R.
; APPLICANT: YONEDA, TOSHIYUKI
; TITLE OF INVENTION: METHODS OF TREATING MULTIPLE MYELOMA AND
; TITLE OF INVENTION: MYELOMA-INDUCED BONE RESORPTION USING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; FILE REFERENCE: A061CIP2
; CURRENT APPLICATION NUMBER: US/10/086,217
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 09/943,659
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/805,840
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US99/21170
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/100,182
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-086-217-6

Query Match 100.0%; Score 23; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
DB 1 EILDV 5

RESULT 2
US-09-320-907B-3
; Sequence 3, Application US/09320907B
; Publication No. US20020198360A1
; GENERAL INFORMATION:
; APPLICANT: GINSBERG, MARK H.
; APPLICANT: PFAFF, MARTIN
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC DOMAINS OF
; TITLE OF INVENTION: TRANSMEMBRANE RECEPTORS
; FILE REFERENCE: SRI-0006
; CURRENT APPLICATION NUMBER: US/09/320,907B
; CURRENT FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 09/187,236
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 5


```
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-569-192-56

Query Match      100.0%; Score 23; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 6
US-10-137-435-14
; Sequence 14, Application US/10137435
; Publication No. US20030013644A1
; GENERAL INFORMATION:
; APPLICANT: Institute of Child Health
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; ENHANCED TRANSESECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; STREET: c/o Institute of Child Health,
; 30 Guildford Street
; CITY: London
; COUNTRY: G.B.
; ZIP: WC1N 1EH
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/137,435
; FILING DATE: 03-May-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656;
; FILING DATE: <Unknown>
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hart, Stephen Lewis
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-137-435-14

Query Match      100.0%; Score 23; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 7
US-09-840-277-95
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```
; Sequence 95, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 95
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-95

Query Match      100.0%; Score 23; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 8
US-09-840-277-96
; Sequence 96, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 96
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-96

Query Match      100.0%; Score 23; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 10 EILDV 14

RESULT 9
US-09-840-277-133
; Sequence 133, Application US/09840277
```

; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHIKO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 133
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-133

Query Match 100.0%; Score 23; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.6; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 10 EILDV 14

RESULT 10
US-09-969-192-57
; Sequence 57, Application US/09969192
; Patent No. US20020151027A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; ROELVINK, PETRUS W.
; KOVESDI, IMRE
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,192
; FILING DATE: 01-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-455061
; FILING DATE: 06-DEC-1999
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-969-192-57

Query Match 100.0%; Score 23; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.5; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 12
US-09-840-277-119

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-969-192-57

Query Match 100.0%; Score 23; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.5; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 11
US-09-969-192-59
; Sequence 59, Application US/09969192
; Patent No. US20020151027A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; ROELVINK, PETRUS W.
; KOVESDI, IMRE
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,192
; FILING DATE: 01-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-455061
; FILING DATE: 06-DEC-1999
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; MOLECULE TYPE: linear
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-969-192-59

Query Match 100.0%; Score 23; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 8.5; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 12
US-09-840-277-119

; Sequence 119, Application US/09840277
; Patent No. US20020168363A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: KOHNO, TADAHITO
; APPLICANT: LACEY, DAVID LEE
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS
; FILE REFERENCE: A-688A
; CURRENT APPLICATION NUMBER: US/09/840,277
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/198,919
; PRIOR FILING DATE: 2000-04-21
; PRIOR APPLICATION NUMBER: 60/201,394
; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Laminin related peptide
US-09-840-277-119

Query Match 100.0%; Score 23; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 11 EILDV 15

RESULT 13

US-09-010-714-11
; Sequence 11, Application US/09010714
; Patent No. US2002012942A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; APPLICANT: Iida, Joji
; TITLE OF INVENTION: POLYPEPTIDES WITH ALPHA 4 INTEGRIN SUBUNIT RELATED
; FILE REFERENCE: 600.332US01
; CURRENT APPLICATION NUMBER: US/09/010,714
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 11
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-010-714-11

Query Match 100.0%; Score 23; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

RESULT 14

US-09-969-192-76
; Sequence 76, Application US/09969192
; Patent No. US20020151027A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: ROELVINK, PETRUS W.
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF

; CONstrained Peptide Motifs
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,192
; FILING DATE: 01-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-455061
; FILING DATE: 06-DEC-1999
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Heftner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 213564
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-09-969-192-76

Query Match 100.0%; Score 23; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 16 EILDV 20

RESULT 15

US-09-925-301-900
; Sequence 900, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P1A106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 900
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-900

Query Match 100.0%; Score 23; DB 10; Length 152;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

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Db      12 EILDV 16
|||||
; SEQ ID NO 5384
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5384

RESULT 16
US-09-738-626-5384
; Sequence 5384, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5384
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5384

Query Match      100.0%; Score 23; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EILDV 5
|||||
Db      118 EILDV 122

RESULT 17
US-09-738-626-4085
; Sequence 4085, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0

Db      304 EILDV 308
|||||
; SEQ ID NO 10394
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10394

Query Match      100.0%; Score 23; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EILDV 5
|||||
Db      304 EILDV 308

RESULT 19
US-09-815-242-13921
; Sequence 13921, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
```



```
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13921
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13921

Query Match 100.0%; Score 23; DB 10; Length 366;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 304 EILDV 308

RESULT 20
US-10-029-654-14
; Sequence 14, Application US/10029654
; Patent No. US20020150958A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim Pharma KG
; TITLE OF INVENTION: Methods for identifying substances for treating
; FILE REFERENCE: 1/1178
; CURRENT APPLICATION NUMBER: US/10/029,654
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/257,878
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 14
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-654-14

Query Match 100.0%; Score 23; DB 12; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 390 EILDV 394

RESULT 21
US-09-925-302-700
; Sequence 700, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-700

Query Match 100.0%; Score 23; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 276 EILDV 280

RESULT 22
US-09-738-626-6313
; Sequence 6313, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIRO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6313
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6313

Query Match 100.0%; Score 23; DB 9; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 47 EILDV 51

RESULT 23
US-09-841-132-492
; Sequence 492, Application US/09841132
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; Patent No. US20020061848A1
; GENERAL INFORMATION:
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C8
; CURRENT APPLICATION NUMBER: US/09/841,132
; CURRENT FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 492
; LENGTH: 560
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(560)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-841-132-492

Query Match 100.0%; Score 23; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 529 EILDV 533

RESULT 24
US-09-738-626-6019
; Sequence 6019, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 6019
; LENGTH: 706
; TYPE: PR1
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6019

Query Match 100.0%; Score 23; DB 9; Length 706;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 600 EILDV 604

RESULT 25
US-09-815-242-13699
; Sequence 13699, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Carr, Grant J.
; APPLICANT: Irawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13699
; LENGTH: 737
; TYPE: PR1
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13699

Query Match 100.0%; Score 23; DB 10; Length 737;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 535 EILDV 539

RESULT 26
US-10-145-014-23
; Sequence 23, Application US/10145014
; Patent No. US20020168755A1
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JB0601QD
; CURRENT APPLICATION NUMBER: US/10/145,014
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/982,308
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-014-23

Query Match 100.0%; Score 23; DB 9; Length 784;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 460 EILDV 464

RESULT 27

US-08-910-386A-9
; Sequence 9, Application US/08910386A
; Patent No. US20020092041A1

; GENERAL INFORMATION:

; APPLICANT: Ronald, Pamela C.

; APPLICANT: Wang, Guo-Liang

; APPLICANT: Song, Wen-Yuang

; APPLICANT: Hulbert, Scot

; APPLICANT: Richter, Todd

; TITLE OF INVENTION: Procedures and Materials for Conferring

; TITLE OF INVENTION: Disease Resistance in Plants

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/910,386A

; FILING DATE: 13-AUG-1997

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Bastian, Kevin L.

; REGISTRATION NUMBER: 34,774

; REFERENCE/DOCKET NUMBER: 023070-058950US

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 813 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-910-386A-9

Query Match 100.0%; Score 23; DB 8; Length 813;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 474 EILDV 478

RESULT 28

US-08-910-386A-5

; Sequence 5, Application US/08910386A

; Patent No. US20020092041A1

; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yuang
; APPLICANT: Hulbert, Scot
; APPLICANT: Richter, Todd
; TITLE OF INVENTION: Procedures and Materials for Conferring
; TITLE OF INVENTION: Disease Resistance in Plants
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,386A
; FILING DATE: 13-AUG-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-058950US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 996 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-910-386A-5

Query Match 100.0%; Score 23; DB 8; Length 996;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EILDV 5
Db 472 EILDV 476

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Job time : 12 secs

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OM protein - protein search, using sw model

'Run on: February 8, 2003, 10:23:08 ; Search time 14 Seconds
(without alignments)
10.508 Million cell updates/sec

Title: US-09-251-073A-16

Perfect score: 23

Sequence: 1 BLDV 5

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Searched: 262574 seqs, 29422922 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 100 summaries

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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	5	1	US-08-109-106-3
2	23	100.0	5	1	US-08-303-162A-3
3	23	100.0	5	1	US-08-634-060-3
4	23	100.0	5	1	US-08-338-282-10
5	23	100.0	5	1	US-08-709-515-3
6	23	100.0	5	2	US-08-700-846-2
7	23	100.0	5	4	US-08-146-503-3
8	23	100.0	5	4	US-08-983-391-2
9	23	100.0	5	4	US-08-498-237-2
10	23	100.0	5	4	US-08-376-372-2
11	23	100.0	5	4	US-08-875-321-2
12	23	100.0	5	5	PCT-US95-07542-3
13	23	100.0	7	2	US-08-701-124-80
14	23	100.0	7	3	US-08-860-248C-50
15	23	100.0	7	3	US-08-860-248C-51
16	23	100.0	7	3	US-08-860-248C-52
17	23	100.0	7	3	US-08-860-248C-53
18	23	100.0	7	4	US-09-130-225-80
19	23	100.0	7	4	US-09-455-061-80
20	23	100.0	8	1	US-07-780-081-1
21	23	100.0	8	1	US-08-158-936-1
22	23	100.0	8	1	US-08-338-282-7
23	23	100.0	8	2	US-08-701-124-56
24	23	100.0	8	2	US-09-025-706-3
25	23	100.0	8	3	US-08-467-580-3
26	23	100.0	8	3	US-09-130-225-56
27	23	100.0	8	4	US-09-025-622-3
28	23	100.0	8	4	US-08-983-391-1
29	23	100.0	8	4	US-08-498-237-1
30	23	100.0	8	4	US-08-376-372-1
31	23	100.0	8	4	US-09-455-061-56
32	23	100.0	8	4	US-09-039-780A-48
33	23	100.0	8	4	US-08-875-321-1
34	23	100.0	8	5	PCT-US95-08516-3
35	23	100.0	10	1	US-08-271-830-101
36	23	100.0	10	1	US-08-435-286-3
37	23	100.0	10	1	US-08-338-282-6
38	23	100.0	10	2	US-08-483-077C-6
39	23	100.0	10	2	US-08-519-109B-6
40	23	100.0	10	3	US-08-923-026-3
41	23	100.0	10	3	US-08-837-154-3
42	23	100.0	10	5	PCT-US94-13943-3
43	23	100.0	10	5	PCT-US95-10811-3
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48	23	100.0	12	1	US-08-338-282-5
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51	23	100.0	12	3	US-08-923-026-2
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55	23	100.0	12	5	US-09-367-953B-25
56	23	100.0	18	4	US-08-701-124-57
57	23	100.0	21	2	US-08-701-124-59
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60	23	100.0	21	4	US-09-455-061-57
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62	23	100.0	21	4	US-08-453-378-2
63	23	100.0	25	1	US-08-391-349A-6
64	23	100.0	25	1	US-07-990-296-4
65	23	100.0	25	1	US-08-190-130-1
66	23	100.0	25	1	US-08-190-130-4
67	23	100.0	25	1	US-08-190-130-4
68	23	100.0	25	1	US-08-435-286-1
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70	23	100.0	25	2	US-08-658-130-20
71	23	100.0	25	2	US-08-483-077C-5
72	23	100.0	25	2	US-08-836-854-2
73	23	100.0	25	2	US-08-480-133A-4
74	23	100.0	25	2	US-08-519-109B-5
75	23	100.0	25	2	US-09-025-706-4
76	23	100.0	25	3	US-08-394-748A-15
77	23	100.0	25	3	US-08-536-891A-2
78	23	100.0	25	3	US-08-923-026-1
79	23	100.0	25	3	US-08-837-154-1
80	23	100.0	25	4	US-09-025-622-4
81	23	100.0	25	4	US-09-039-780A-17
82	23	100.0	25	4	US-09-366-009-2
83	23	100.0	25	5	PCT-US93-11781-4
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87	23	100.0	25	5	PCT-US96-08723-20
88	23	100.0	27	4	US-08-983-391-4
89	23	100.0	31	1	US-08-875-321-4
90	23	100.0	31	1	US-08-190-130-5
91	23	100.0	34	2	US-08-701-124-76
92	23	100.0	34	3	US-09-130-225-76
93	23	100.0	34	4	US-09-455-061-76
94	23	100.0	36	1	US-08-303-162A-22
95	23	100.0	36	1	US-08-634-060-22
96	23	100.0	36	1	US-08-709-515-22
97	23	100.0	46	1	US-08-338-282-1
98	23	100.0	50	4	US-09-039-780A-49
99	23	100.0	67	4	US-09-039-780A-43
100	23	100.0	70	4	US-09-039-780A-50

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Sequence 49, Appl
Sequence 43, Appl
Sequence 50, Appl

ALIGNMENTS

RESULT 1
US-08-109-106-3
; Sequence 3, Application US/08109106
; Patent No. 5475100
; GENERAL INFORMATION:
; APPLICANT: Kimikazu HASHINO et al.
; TITLE OF INVENTION: Artificial Antibody
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Menderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/109,106
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/725,668
; FILING DATE: July 3, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX: 202-371-8856
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:

; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-109-106-3
Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
|
Db 1 EILDV 5
|
RESULT 2
US-08-303-162A-3
; Sequence 3, Application US/08303162A
; Patent No. 5559099
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Brough, Douglas E.
; APPLICANT: McVey, Duncan L.
; APPLICANT: Bruder, Joseph T.
; TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303,162A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr.
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 61306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-303-162A-3
Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EILDV 5
|
|
|
|

Db 1 EILDV 5

RESULT 3
US-08-634-060-3
; Sequence 3, Application US/08634060
; Patent No. 5712136
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Roelivink, Petrus W.
; TITLE OF INVENTION: ADENOVIRUS-MEDIATED CELL TARGETING COMMANDED BY
; TITLE OF INVENTION: THE ADENOVIRUS PENTON BASE PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,060
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,162
; FILING DATE: 08-SEP-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr. 30763
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 71602
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-634-060-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 4
US-08-338-282-10
; Sequence 10, Application US/08338282
; Patent No. 5730978
; GENERAL INFORMATION:
; APPLICANT: Wayner, E.A.
; TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA

ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,282
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/814,873
; FILING DATE: December 24, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/402,389
; FILING DATE: September 1, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundemo, John, S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: CYTE-1-6162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: EILDV
US-08-338-282-10

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 5
US-08-709-515-3
; Sequence 3, Application US/08709515
; Patent No. 5731190
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Kovesdi, Imre
; APPLICANT: Brough, Douglas S.
; APPLICANT: McVey, Duncan L.
; APPLICANT: Bruder, Joseph T.
; TITLE OF INVENTION: CHIMERIC PENTON BASE MOLECULES
; TITLE OF INVENTION: AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,515
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,162

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; FILING DATE: 08-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr. 30763
; REGISTRATION NUMBER: 73845
; REFERENCE/DOCKET NUMBER: 73845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-709-515-3

Query Match 100.0%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 6
US-08-700-846-2
; Sequence 2, Application US/08700846
; Patent No. 5962311
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: ROELVINK, PETRUS W.
; TITLE OF INVENTION: A SHORT-SHAFTED ADENOVIRAL FIBER AND ITS
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LEYDIG, VOIT & MAYER, LTD.
; STREET: TWO PRUDENTIAL PLAZA, SUITE 4900
; CITY: CHICAGO
; STATE: IL
; COUNTRY: USA
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/700,846
; APPLICATION NUMBER: US/08/700,846
; FILING DATE: 21-AUG-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: LARCHER, CAROL
; REGISTRATION NUMBER: 35243
; REFERENCE/DOCKET NUMBER: 74294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-700-846-2

Query Match 100.0%; Score 23; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; FILING DATE: 08-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk, John Jr. 30763
; REGISTRATION NUMBER: 73845
; REFERENCE/DOCKET NUMBER: 73845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-146-503-3

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 7
US-09-146-503-3
; Sequence 3, Application US/09146503
; Patent No. 6184206
; GENERAL INFORMATION:
; APPLICANT: Jeffrey W. Smith
; APPLICANT: Dana D. Hu
; TITLE OF INVENTION: Integrin Ligand Dissociators
; FILE REFERENCE: 02046.0002
; CURRENT APPLICATION NUMBER: US/09/146,503
; CURRENT FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/057,463
; EARLIER FILING DATE: 1997-09-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-146-503-3

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 8
US-08-983-391-2
; Sequence 2, Application US/08983391
; Patent No. 6239108
; GENERAL INFORMATION:
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Adams, Steven P.
; APPLICANT: Castro, Alfredo C.
; APPLICANT: Zimmerman, Craig N.
; APPLICANT: Cuervo, Julio Herman
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Hammond, Charles E.
; APPLICANT: Carter, Mary Beth
; APPLICANT: Almquist, Ronald G.
; APPLICANT: Ensinger, Carol Lee
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; FILE REFERENCE: 10274/024002
; CURRENT APPLICATION NUMBER: US/08/983,391
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 96/11570
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: US 08/498,237
; PRIOR FILING DATE: 1995-07-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated protein
; US-08-983-391-2

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 BILDV 5
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Db 1 BILDV 5

RESULT 9
US-08-498-237-2
; Sequence 2, Application US/08498237
; Patent No. 6248713
; GENERAL INFORMATION:
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Adams, Steven P
; APPLICANT: Castro, Alfredo C
; APPLICANT: Zimmerman, Craig N
; APPLICANT: Cuervo, Julio H
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Hammond, Charles E
; APPLICANT: Carter, Mary B
; APPLICANT: Almquist, Ronald G
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/498,237
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-498-237-2

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
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Db 1 BILDV 5

RESULT 10
US-08-376-372-2
; Sequence 2, Application US/08376372
; Patent No. 6306840
; GENERAL INFORMATION:
; APPLICANT: Adams, Steven P
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Lee, Wen-Cherng

; APPLICANT: Castro, Alfredo C
; APPLICANT: Zimmerman, Craig N
; APPLICANT: Hammond, Charles E
; APPLICANT: Liao, Yu-Sheng
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/376,372
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: B180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-376-372-2

Query Match 100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
|||||
Db 1 BILDV 5

RESULT 11
US-08-875-321-2
; Sequence 2, Application US/08875321
; Patent No. 6376538
; GENERAL INFORMATION:
; APPLICANT: Adams, Steven P.
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Castro, Alfredo C.
; APPLICANT: Zimmerman, Craig N.
; APPLICANT: Hammond, Charles E.
; APPLICANT: Liao, Yu-Sheng
; APPLICANT: Cuervo, Julio Hernan
; APPLICANT: Singh, Juswinder
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; FILE REFERENCE: 10274-023002
; CURRENT APPLICATION NUMBER: US/08/875,321
; CURRENT FILING DATE: 1997-09-27
; PRIOR APPLICATION NUMBER: US 08/376, 372
; PRIOR FILING DATE: 1995-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-2

Query Match      100.0%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 12
PCT-US95-07542-3
; Sequence 3, Application PC/TUS9507542
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: STRUCTURAL MODELS FOR CYTOPLASMIC
; TITLE OF INVENTION: DOMAINS OF TRANSMEMBRANE RECEPTORS
; NUMBER OF SEQUENCES: 20
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07542
; FILING DATE: 13-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/260,514
; FILING DATE: 15-JUN-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Ligand sequence recognized by integrin
PCT-US95-07542-3

Query Match      100.0%; Score 23; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 13
US-08-701-124-80
; Sequence 80, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
us-09-251-073a-16.open.ra1

Query Match      100.0%; Score 23; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 14
US-08-860-248C-50
; Sequence 50, Application US/08860248C
; Patent No. 6034056
; GENERAL INFORMATION:
; APPLICANT: DUTTA, Anand
; TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 122
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS WORD
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,248C
; FILING DATE: 24-JUNE-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9426254.0
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9505905.1
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9513904.4
; FILING DATE: 07-JUL-1995
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 7
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "3-AMINO-PROPIONIC ACID"
US-08-860-248C-50

Query Match      100.0%; Score 23; DB 3; Length 7;
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Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 15
US-08-860-248C-51
Sequence 51, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 51
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 7
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "5-AMINO-PENTANOIC ACID"
US-08-860-248C-51

Query Match 100.0%; Score 23; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 16
US-08-860-248C-52
Sequence 52, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9505905.1
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9513904.4
FILING DATE: 07-JUL-1995
INFORMATION FOR SEQ ID NO: 52
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 7
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "6-AMINO-HEXANOIC ACID"
US-08-860-248C-52

Query Match 100.0%; Score 23; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 17
US-08-860-248C-53
Sequence 53, Application US/08860248C
Patent No. 6034056
GENERAL INFORMATION:
APPLICANT: DUTTA, Anand
TITLE OF INVENTION: FIBRONECTIN ADHESION INHIBITORS
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,248C
FILING DATE: 24-JUNE-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9426254.0

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;
; FILING DATE: 24-DEC-1994
; PRIOR APPLICATION DATA: GB 9505905.1
; FILING DATE: 23-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9513904.4
; FILING DATE: 07-JUL-1995
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 7
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "8-AMINO-OCTANOIC ACID"
US-08-860-248C-53

Query Match 100.0%; Score 23; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 18
US-09-130-225-80
; Sequence 80, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,225
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-130-225-80

Query Match 100.0%; Score 23; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 19
US-09-455-061-80
; Sequence 80, Application US/09455061
; Patent No. 6329190
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/455,061
; FILING DATE: 06-DEC-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 203128
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-455-061-80

Query Match 100.0%; Score 23; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 20
US-07-780-081-1
; Sequence 1, Application US/07780081
; Patent No. 5229366
; GENERAL INFORMATION:
; APPLICANT: TSUKADA, Yoshihisa
; APPLICANT: ORIKASA, Atsushi
; TITLE OF INVENTION: PEPTIDE-CONTAINING POLYETHYLENE GLYCOL
; DERIVATIVES AND APPLICATION THEREOF
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak and Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
```

Qy 1 EILDV 5

COUNTRY: USA
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/780,081
FILING DATE: 19911021
CLASSIFICATION: 530
TELEPHONE: 202-293-7060
TELEFAX: 202-293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-780-081-1

Query Match 100.0%; Score 23; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 21
US-08-158-936-1
Sequence 1, Application US/08158936
Patent No. 5521067
GENERAL INFORMATION:
APPLICANT: Seshi, Beereilli
TITLE OF INVENTION: Bone Marrow Cell Adhesion Molecules and
TITLE OF INVENTION: Process for Detecting Adherence Between Cell Adhesion
TITLE OF INVENTION: Molecules and Cells Generally
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/158,936
FILING DATE: No. 5521067ember 24, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 176/60030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
US-08-158-936-1

Query Match 100.0%; Score 23; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 22
US-08-338-282-7
Sequence 7, Application US/08338282
Patent No. 5730978
GENERAL INFORMATION:
APPLICANT: Wayner, E.A.
TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Sundsmo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: EILDV PST
US-08-338-282-7

Query Match 100.0%; Score 23; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 23
US-08-701-124-56
Sequence 56, Application US/08701124
Patent No. 5846782
GENERAL INFORMATION:

;; APPLICANT: Wickham, Thomas J.
;; APPLICANT: Roelvink, Petrus W.
;; APPLICANT: Kovesdi, Imre
;; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
;; STRANDEDNESS: 80
;; NUMBER OF SEQUENCES: 80
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
;; STREET: Two Prudential Plaza - 49th Floor
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60601
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/701.124
;; FILING DATE: 21-AUG-1996
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-701-124-56
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 1 EILDV 5
RESULT 24
US-09-025-706-3
; Sequence 3, Application US/09025706
; Patent No. 5958874
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Greiling, Doris
; APPLICANT: Gailit, James
; TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
; TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025.706
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133

;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-025-706-3
Query Match 100.0%; Score 23; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 1 EILDV 5
RESULT 25
US-08-467-580-3
; Sequence 3, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: derived from fibronectin
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: ACETYLTATION
; US-08-467-580-3
Query Match 100.0%; Score 23; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 1 EILDV 5
RESULT 26
US-09-130-225-56
; Sequence 56, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

```
;
;
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,225
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-130-225-56
;
Query Match 100.0%; Score 23; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 27
US-09-025-622-3
; Sequence 3, Application US/09025622
; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Greiling, Doris
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaecle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-025-622-3
;
Query Match 100.0%; Score 23; DB 4; Length 8;
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Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 28
US-08-983-391-1
; Sequence 1, Application US/08983391
; Patent No. 6239108
; GENERAL INFORMATION:
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Adams, Steven P.
; APPLICANT: Castro, Alfredo C.
; APPLICANT: Zimmerman, Craig N.
; APPLICANT: Cuervo, Julio Herman
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Hammond, Charles E.
; APPLICANT: Carter, Mary Beth
; APPLICANT: Almquist, Ronald G.
; APPLICANT: Ensinger, Carol Lee
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; FILE REFERENCE: 10274/024002
; CURRENT APPLICATION NUMBER: US/08/983,391
; CURRENT FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 96/11570
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: US 08/498,237
; PRIOR FILING DATE: 1995-07-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated protein
;
US-08-983-391-1
;
Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 29
US-08-498-237-1
; Sequence 1, Application US/08498237
; Patent No. 6248713
; GENERAL INFORMATION:
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Adams, Steven P
; APPLICANT: Castro, Alfredo C
; APPLICANT: Zimmerman, Craig N
; APPLICANT: Cuervo, Julio H
; APPLICANT: Lee, Wen-Cherng
; APPLICANT: Hammond, Charles E
; APPLICANT: Carter, Mary B
; APPLICANT: Almquist, Ronald G
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498,237
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-498-237-1

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 30
US-08-376-372-1
Sequence 1, Application US/08376372
Patent No. 6306840
GENERAL INFORMATION:
APPLICANT: Adams, Steven P
APPLICANT: Lin, Ko-Chung
APPLICANT: Lee, Wen-Cheng
APPLICANT: Castro, Alfredo C
APPLICANT: Zimmerman, Craig N
APPLICANT: Hammond, Charles E
APPLICANT: Liao, Yu-Sheng
TITLE OF INVENTION: CELL ADHESION INHIBITORS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/376,372
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B180
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090

TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-376-372-1

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 31
US-09-455-061-56
Sequence 56, Application US/09455061
Patent No. 6329190
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,061
FILING DATE: 06-DEC-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 203128
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-455-061-56

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 32
US-09-039-780A-48
; Sequence 48, Application US/09039780A
; Patent No. 6376248
; GENERAL INFORMATION:
; APPLICANT: HAWLEY-NELSON, PAMELA
; SHIH, POEN
; JESSE, JOEL A.
; SCHIFFERLI, KEVIN P.
; GEBEYERU, GULILAT
; TITLE OF INVENTION: PEPTIDE-ENHANCED TRANSFECTIONS
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREENLEE, WINNER & SULLIVAN
; STREET: 5370 MANHATTAN CIRCLE, SUITE 201
; CITY: BOULDER
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,780A
; FILING DATE: 16-Mar-1998
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SULLIVAN, SALLY A.
; REGISTRATION NUMBER: 32,064
; REFERENCE/DOCKET NUMBER: 32-95C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303)499-8080
; TELEFAX: (303)499-8089
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-039-780A-48

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
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|
|
Db 1 EILDV 5

RESULT 33
US-08-875-321-1
; Sequence 1, Application US/08875321
; Patent No. 6376538
; GENERAL INFORMATION:
; APPLICANT: Adams, Steven P.
; APPLICANT: Lin, Ko-Chung
; APPLICANT: Lee, Wen-Cheng
; APPLICANT: Castro, Alfredo C.
; APPLICANT: Zimmerman, Craig N.
; APPLICANT: Hammond, Charles E.
; APPLICANT: Liao, Yu-Sheng
; APPLICANT: Cuervo, Julio Hernan
; TITLE OF INVENTION: CELL ADHESION INHIBITORS
; FILE REFERENCE: 10274-023002
; CURRENT APPLICATION NUMBER: US/08/875,321
; CURRENT FILING DATE: 1997-09-27

; PRIOR APPLICATION NUMBER: US 08/376, 372
; PRIOR FILING DATE: 1995-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-08-875-321-1

Query Match 100.0%; Score 23; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
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|
|
Db 1 EILDV 5

RESULT 34
PCT-US95-08516-3
; Sequence 3, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATHENA NEUROSCIENCES, INC.
; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
; STREET: 800 Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08516
; FILING DATE: 10-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/273,055
; FILING DATE: 11-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOL, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 002010-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-3620
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-08516-3

Query Match 100.0%; Score 23; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 1 EILDV 5

RESULT 35
US-08-271-830-101

; Sequence 101, Application US/08271830
; Patent No. 5510332
; GENERAL INFORMATION:
; APPLICANT: Kogan, Timothy P.
; APPLICANT: Ren, Kaijun
; APPLICANT: Vanderslice, Peter
; APPLICANT: Beck, Pamela J.
; TITLE OF INVENTION: A PROCESS OF INHIBITING THE BINDING OF THE
; TITLE OF INVENTION: INTEGRIN '4.1 TO VCAM OR FIBRONECTIN AND
; TITLE OF INVENTION: LINEAR PEPTIDES THEREFOR
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 5510332th Stetson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271.830
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5510332thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 101:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /label=Xaa
; OTHER INFORMATION: /note="Xaa=Thr-NH2."
US-08-271-830-101

Query Match 100.0%; Score 23; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 36
US-08-435-286-3
; Sequence 3, Application US/08435286
; Patent No. 5688913
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 5688913th Stetson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: US/08/164,101
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-286-3

Query Match 100.0%; Score 23; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 37
US-08-338-282-6
; Sequence 6, Application US/08338282
; Patent No. 5730978
; GENERAL INFORMATION:
; APPLICANT: Wayner, E.A.
; TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,282
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: 07/814,873
; FILING DATE: December 24, 1991
; PRIOR APPLICATION DATA: 07/402,389
; FILING DATE: September 1, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundsmo, John, S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: CYTE-1-6162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: GPRIL DVPST
US-08-338-282-6

Query Match      100.0%; Score 23; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 38
US-08-483-077C-6
; Sequence 6, Application US/08483077C
; Patent No. 5811391
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; COMPOSITIONS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,077C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1647
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-077C-6

Query Match      100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 39
US-08-519-109B-6
; Sequence 6, Application US/08519109B
; Patent No. 5869448
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; COMPOSITIONS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,109B
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-519-109B-6

Query Match      100.0%; Score 23; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 40
US-08-923-026-3
; Sequence 3, Application US/08923026
; Patent No. 6103870
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 6103870th Stetson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/923,026
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,101
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-923-026-3

Query Match 100.0%; Score 23; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||
Db 3 EILDV 7

RESULT 41

US-08-837-154-3
; Sequence 3, Application US/08837154
; Patent No. 6117840

; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS
; AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Welsh & Katz, Ltd.
; STREET: 135 South La Salle Street, Suite 1625
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,154
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)781-9470
; TELEFAX: (312)781-9548
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-837-154-3

Query Match 100.0%; Score 23; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||
Db 3 EILDV 7

RESULT 42

PCT-US94-13943-3
; Sequence 3, Application PC/TUS9413943
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13943
; FILING DATE: 5-DEC-1994
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-13943-3

Query Match 100.0%; Score 23; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||
Db 3 EILDV 7

RESULT 43

PCT-US95-10811-3
; Sequence 3, Application PC/TUS9510811
; GENERAL INFORMATION:
; APPLICANT: Cytel Corporation
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics, Compositions and Methods For Using The Same
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10811
; FILING DATE: 25-AUG-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hook, Gregory R.
; REGISTRATION NUMBER: 38,701
; REFERENCE/DOCKET NUMBER: FP-CY 1778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids

```
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-10811-3

Query Match      100.0%; Score 23; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
   |||||
Db 3 BILDV 7

RESULT 44
US-08-467-580-2
; Sequence 2, Application US/08467580B
; Patent No. 6001809
; GENERAL INFORMATION:
; APPLICANT: Thorsett, Eugene D
; APPLICANT: Yednock, Theodore A
; APPLICANT: Pleiss, Michael A
; TITLE OF INVENTION: Inhibitors of Leukocyte Adhesion
; FILE REFERENCE: 123-US-CIP1
; CURRENT APPLICATION NUMBER: US/08/467,580B
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/273,055
; EARLIER FILING DATE: 1994-07-11
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide
; OTHER INFORMATION: derived from fibronectin
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: ACETYLATION
US-08-467-580-2

Query Match      100.0%; Score 23; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
   |||||
Db 4 BILDV 8

RESULT 45
PCT-US95-08516-2
; Sequence 2, Application PC/TUS9508516
; GENERAL INFORMATION:
; APPLICANT: ATHENA NEUROSCIENCES, INC.
; TITLE OF INVENTION: INHIBITORS OF LEUKOCYTE ADHESION
; NUMBER OF SEQUENCES: 157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ATHENA NEUROSCIENCES, INC.
; STREET: 800 Gateway Blvd.
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08516

;
; FILING DATE: 10-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/273,055
; FILING DATE: 11-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MOOI, LESLIE A.
; REGISTRATION NUMBER: 37,047
; REFERENCE/DOCKET NUMBER: 002010-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 877-0900
; TELEFAX: (415) 877-3620
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-08516-2

Query Match      100.0%; Score 23; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
   |||||
Db 4 BILDV 8

RESULT 46
US-08-190-130-3
; Sequence 3, Application US/08190130
; Patent No. 5628979
; GENERAL INFORMATION:
; APPLICANT: STUTTLE, Alan William John
; TITLE OF INVENTION: No. 5628979el Reagent For Tumour
; TITLE OF INVENTION: Imaging and Therapy
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 720 Kb storable
; COMPUTER: IBM PS/2, Model 35 SX
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,130
; FILING DATE: June 13, 1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Minnich, Richard J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: YOU 2 042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666
; TELEX: (216) 980162
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-190-130-3
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```
Query Match          100.0%; Score 23; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 47
US-08-435-286-2
; Sequence 2, Application US/08435286
; Patent No. 568913
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 568913th Stetson, Suite 4700
; City: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,101
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)616-5400
; TELEFAX: (312)616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-286-2

Query Match          100.0%; Score 23; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 48
US-08-338-282-5
; Sequence 5, Application US/08338282
; Patent No. 5730978
; GENERAL INFORMATION:
; APPLICANT: Wayner, E.A.
; TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
```

```
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,282
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/814,873
FILING DATE: December 24, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/402,389
FILING DATE: September 1, 1989
ATTORNEY/AGENT INFORMATION:
NAME: Sundemo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: CYTE-1-6162
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: B12; Fig. 9B; LHGPE ILDVP ST
US-08-338-282-5

Query Match          100.0%; Score 23; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 49
US-08-483-077C-9
; Sequence 9, Application US/08483077C
; Patent No. 5811391
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
```

```

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1647
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-483-077C-9

Query Match 100.0%; Score 23; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 50
US-08-519-109B-9
; Sequence 9, Application US/08519109B
; Patent No. 5869448
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,109B
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-8949
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-519-109B-9

Query Match 100.0%; Score 23; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5

; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1647
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-483-077C-9

Query Match 100.0%; Score 23; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 51
US-08-923-026-2
; Sequence 2, Application US/08923026
; Patent No. 6103870
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 6103870th Stetson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,026
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,101
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5400
; TELEFAX: (312) 616-5460
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-923-026-2

Query Match 100.0%; Score 23; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 5 EILDV 9

RESULT 52
US-08-837-154-2
; Sequence 2, Application US/08837154
; Patent No. 6117840
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS
; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weleth & Katz, Ltd.
; STREET: 135 South La Salle Street, Suite 1625
; CITY: Chicago
; STATE: IL
```

```
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,154
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)781-9470
; TELEFAX: (312)781-9548
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-837-154-2
Query Match 100.0%; Score 23; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 5 EILDV 9
RESULT 53
US-09-424-656-14
; Sequence 14, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-424-656-14
Query Match 100.0%; Score 23; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 5 EILDV 9
RESULT 54
US-09-424-656-14
; Sequence 14, Application US/09424656
; Patent No. 6458026
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INTEGRIN-TARGETING VECTORS HAVING
; ENHANCED TRANSFECTION ACTIVITY
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/424,656
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9711115.7
; FILING DATE: 29-MAY-1997
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-424-656-14
Query Match 100.0%; Score 23; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 5 EILDV 9
RESULT 55
PCT-US94-13943-2
; Sequence 2, Application PC/TUS9413943
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13943
; FILING DATE: 5-DEC-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-13943-2
Query Match 100.0%; Score 23; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EILDV 5
Db 5 EILDV 9
RESULT 55
PCT-US95-10811-2
; Sequence 2, Application PC/TUS9510811
; GENERAL INFORMATION:
; APPLICANT: Cytel Corporation
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; Compositions and Methods For Using The Same
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10811
; FILING DATE: 25-AUG-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Hook, Gregory R.
; REGISTRATION NUMBER: 38,701
; REFERENCE/DOCKET NUMBER: FP-CY 1778
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-10811-2
Query Match 100.0%; Score 23; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 12;
```


Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 5 EILDV 9

RESULT 56

US-09-367-953B-25
; Sequence 25, Application US/09367953B
; Patent No. 6287572
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J
; APPLICANT: Kingsman, Susan M
; TITLE OF INVENTION: Anti-HIV peptides and proteins
; FILE REFERENCE: 550-154
; CURRENT APPLICATION NUMBER: US/09/367,953B
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/GB98/00563
; PRIOR FILING DATE: 1998-02-23
; PRIOR APPLICATION NUMBER: GB 9703802.0
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Linker
US-09-367-953B-25

Query Match 100.0%; Score 23; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 5 EILDV 9

RESULT 57

US-08-701-124-57
; Sequence 57, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/701,124
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-701-124-57

Query Match 100.0%; Score 23; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 1 EILDV 5

RESULT 58

US-08-701-124-59
; Sequence 59, Application US/08701124
; Patent No. 5846782
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/701,124
; APPLICATION NUMBER: US/08/701,124
; FILING DATE: 21-AUG-1996
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-701-124-59

Query Match 100.0%; Score 23; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|
|
|
|
Db 3 EILDV 7

RESULT 59

US-09-130-225-57
; Sequence 57, Application US/09130225
; Patent No. 6057155
; GENERAL INFORMATION:
; APPLICANT: Wickham, Thomas J.
; APPLICANT: Roelvink, Petrus W.
; APPLICANT: Kovesdi, Imre
; TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
; TITLE OF INVENTION: CONSTRAINED PEPTIDE MOTIFS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza - 49th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-225-57

Query Match 100.0%; Score 23; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 60
US-09-130-225-59
Sequence 59, Application US/09130225
Patent No. 6057155
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,225
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-225-59

Query Match 100.0%; Score 23; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 3 EILDV 7

RESULT 61
US-09-455-061-57
Sequence 57, Application US/09455061
Patent No. 6329190
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/455,061
FILING DATE: 06-DEC-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 9-130225
FILING DATE: 06-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 8-701124
FILING DATE: 21-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hefner, M. Daniel
REGISTRATION NUMBER: 41,826
REFERENCE/DOCKET NUMBER: 203128
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-455-061-57

Query Match 100.0%; Score 23; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 1 EILDV 5

RESULT 62
US-09-455-061-59
Sequence 59, Application US/09455061
Patent No. 6329190
GENERAL INFORMATION:
APPLICANT: Wickham, Thomas J.
APPLICANT: Roelvink, Petrus W.
APPLICANT: Kovesdi, Imre
TITLE OF INVENTION: TARGETING ADENOVIRUS WITH USE OF
CONSTRAINED PEPTIDE MOTIFS
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza - 49th Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA

```
;
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/455.061
; FILING DATE: 06-DEC-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 9-130225
; FILING DATE: 06-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 8-701124
; FILING DATE: 21-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hefner, M. Daniel
; REGISTRATION NUMBER: 41,826
; REFERENCE/DOCKET NUMBER: 203128
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-455-061-59

Query Match 100.0%; Score 23; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 3 BILDV 7

RESULT 63
US-08-453-378-2
; Sequence 2, Application US/08453378
; Patent No. 5616468
; GENERAL INFORMATION:
; APPLICANT: Salmi, Marko
; APPLICANT: Jalakanen, Sirpa
; TITLE OF INVENTION: Compositions And Diagnostic Methods
; TITLE OF INVENTION: Using Monoclonal Antibodies Against CD44v6
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453.378
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/078,063
; FILING DATE: 18-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: 1102.0070000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 2:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-453-378-2

Query Match 100.0%; Score 23; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 17 BILDV 21

RESULT 64
US-08-291-349A-6
; Sequence 6, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291.349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-25
; OTHER INFORMATION: /note= "Fm6 (1961-1985)
; OTHER INFORMATION: fibronectin fragment : CS-1"
; US-08-291-349A-6

Query Match 100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
```

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Db 18 EILDV 22
|||||
RESULT 65
US-07-990-296-4
; Sequence 4, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: Allen, Janice B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; TITLE OF INVENTION: With Fibronection Activity
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/990,296
; FILING DATE: 19921210
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600.252-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Fragment of the 33 kD carboxy
; NAME/KEY: terminal heparin-binding fragment of the A
; NAME/KEY: chain of fibronection
; LOCATION: Represents isolated fibronection
; LOCATION: residues 1961-1985 from the A chain of human
; LOCATION: plasma fibronection
; US-07-990-296-4
;
Query Match 100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 18 EILDV 22

RESULT 66
US-08-190-130-1
; Sequence 1, Application US/08190130
; Patent No. 5628979
; GENERAL INFORMATION:
; APPLICANT: STUTTLE, Alan William John
; TITLE OF INVENTION:
; TITLE OF INVENTION: No. 5628979el Reagent For Tumour
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 720 Kb, storable
; COMPUTER: IBM PS/2, Model 35 SX
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,130
; FILING DATE: June 13, 1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Minnich, Richard J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: YOU 2 042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666
; TELEX: (216) 980162
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; US-08-190-130-1
;
Query Match 100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
|||||
Db 18 EILDV 22

RESULT 67
US-08-190-130-4
; Sequence 4, Application US/08190130
; Patent No. 5628979
; GENERAL INFORMATION:
; APPLICANT: STUTTLE, Alan William John
; TITLE OF INVENTION:
; TITLE OF INVENTION: No. 5628979el Reagent For Tumour
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fay, Sharpe, Beall, Fagan,
; ADDRESSEE: Minnich & McKee
; STREET: 1100 Superior Avenue
; STREET: Suite 700
; CITY: Cleveland
; STATE: Ohio
; COUNTRY: U.S.A.
; ZIP: 44114-2518
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch,
; MEDIUM TYPE: 720 Kb, storable
; COMPUTER: IBM PS/2, Model 35 SX
; OPERATING SYSTEM: DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,130
```

; FILING DATE: June 13, 1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Minnich, Richard J.
; REGISTRATION NUMBER: 24,175
; REFERENCE/DOCKET NUMBER: YOU 2 042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (216) 861-5582
; TELEFAX: (216) 241-1666
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-190-130-4

Query Match 100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

RESULT 68
US-08-435-286-1
; Sequence 1, Application US/08435286
; Patent No. 5688913
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Gaeta, Federico C.A.
; TITLE OF INVENTION: CS-1 PEPTIDOMIMETICS, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Goldsmith, Shore & Milnamow, Ltd.
; STREET: 180 No. 5688913th Stetson, Suite 4700
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,286
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,101
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gamson, Edward P.
; REGISTRATION NUMBER: 29,381
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5400
; TELEFAX: (312) 616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-435-286-1

Query Match 100.0%; Score 23; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

RESULT 69
US-08-338-282-2
; Sequence 2, Application US/08338282
; Patent No. 5730978
; GENERAL INFORMATION:
; APPLICANT: Wayner, E.A.
; TITLE OF INVENTION: INHIBITION OF LYMPHOCYTE ADHERENCE TO VASCULAR ENDOTHELIUM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 2800 Pacific First Center, 1420 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/338,282
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/814,873
; FILING DATE: December 24, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/402,389
; FILING DATE: September 1, 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sundemo, John S.
; REGISTRATION NUMBER: 34,446
; REFERENCE/DOCKET NUMBER: CYTE-1-6162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
; TELEFAX: 1-206-224-0779
; TELEX: 4938023
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: CS-1 domain; Fig. 9A; DELPQ LVTLP HPNLH GPETL DVPST
US-08-338-282-2

Query Match 100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

RESULT 70
US-08-658-130-20
; Sequence 20, Application US/08658130
; Patent No. 5736392
; GENERAL INFORMATION:
; APPLICANT: Hawley-Nelson, Pamela
; APPLICANT: Lan, Jjiang
; APPLICANT: Shih, PoJen
; APPLICANT: Jessee, Joel A.

APPLICANT: Shifferli, Kevin P.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,130
FILING DATE: 04-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 32-95A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-658-130-20

Query Match 100.0%; Score 23; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

RESULT 71
US-08-483-077C-5
Sequence 5, Application US/08483077C
Patent No. 5811391
GENERAL INFORMATION:
APPLICANT: Arrhenius, Thomas S.
APPLICANT: Tempczyk, Anna
APPLICANT: Ellices, Mariano J.
APPLICANT: Zheng, Zhong-Li
TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
TITLE OF INVENTION: Compositions and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,077C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-CY 1647
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-077C-5

Query Match 100.0%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

RESULT 72
US-08-836-854-2
Sequence 2, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSPECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
US-08-836-854-2

Query Match      100.0%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 18 BILDV 22

RESULT 73
US-08-480-133A-4
; Sequence 4, Application US/08480133A
; Patent No. 5840691
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: McCarthy, James B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: Allen, Janice B.
; APPLICANT: Billups, Kevin L.
; APPLICANT: Everett, Jeffrey E.
; TITLE OF INVENTION: Method for Treating Inflammatory
; DISEASES Using Polypeptides with Fibronectin Activity
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 90 South 7th Street, 3100 No. 5840691west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,133A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/139,903
; FILING DATE: 21-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,296
; FILING DATE: 10-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 600-308US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-480-133A-4

Query Match      100.0%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 18 BILDV 22

RESULT 74
US-08-519-109B-5
; Sequence 5, Application US/08519109B
; Patent No. 5869448
; GENERAL INFORMATION:
; APPLICANT: Arrhenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; Compositions and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,109B
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-519-109B-5

Query Match      100.0%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BILDV 5
Db 18 BILDV 22

RESULT 75
US-09-025-706-4
; Sequence 4, Application US/09025706
; Patent No. 5958874
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Greiling, Doris
; APPLICANT: Gallit, James
; TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
; EXTRACELLULAR MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Muegel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/025,706
; APPLICATION NUMBER: US/09/025,706
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-706-4

Query Match 100.0%; Score 23; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EILDV 5
Db 18 EILDV 22

Search completed: February 8, 2003, 10:25:20
Job time : 16 secs
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